

## FIGURE 1

CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG  
AGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA  
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT  
TCTGGTGTGTCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT  
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCC  
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTATAGGACCGCCTAC  
CGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG  
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG  
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG  
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC  
CGGCAGTTACTGGTGCCAGTGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG  
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAG  
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT  
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC  
TCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTC  
CTGGAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGACTCGTGA<sup>1</sup>CTGCCAGCGCCCCAGG  
CTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTC  
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCTCCTC  
CCCTTCCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT  
CCACCCCTGGCTACCCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA  
GCTGAGGGAAGGTACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC  
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAATGAAA  
CGTGAAGGGCGGCCGCGACTCT  
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT  
TACAAAT

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## **FIGURE 2**

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV  
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC  
GAAICQPPCRNGGSCVQPGRRCRCPAGWRGDTCSQSDVDECSARRGGCPQRCINTAGSYWCQCW  
EGHSLSADGTL CVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS  
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 93-97, 270-274

### **N-myristoylation sites.**

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,  
191-197, 265-271

### **Amidation site.**

amino acids 26-30

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 152-164

### **Cell attachment sequence.**

amino acids 130-133

### **EGF-like domain cysteine pattern signature.**

amino acids 123-135

### FIGURE 3

CGCTCGCCCCGTCGCCCCCTCGCCTCCCCGCGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG  
GTCAGCCACGGCGGGGACTATGGGTGAAATTCCCGGCGCTCACGCACTACTGGCCCCCTGATC  
CGGTTCTTGGTGCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA  
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT  
ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGTTT  
GTGAACAGCAAGAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGTGGCAGGGGCCATCGC  
TGCCGTCTTTTACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC  
ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCTTT  
CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT  
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC  
TTCACAGTCACCTGGAATGCCGGGAGCCCCTGCTCATCCCGATCCTCTCCTTGTACATGGGC  
GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTACGACATCATCCC  
TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT  
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCCGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTACATGCCATAACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG  
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC  
ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTTCTTTGCGGATCTTCTCCTTCTTCCAGTTCCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCCTTGCCCCCAGCTCTGTGCTGCG  
GATCATCGTCCTCATCGCCAGCCTCGTGGTCCTACCCTACCTGGGGGTGCACGGTGCGACCC  
TGGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTCGCCATCGCTGCG  
TGCTATGTCTACCGGAAGCAGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA  
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAATGAGAGAGG  
AGAATGAATAAGGCACGGGACGCCATGGGCACCTGCAGGGACGGTCAGTCAGGATGACACTTC  
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTTTGTTTTGTTTTGGTAAT  
GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT  
GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC  
TTCATAACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC  
TCCTCCCCTGGACAATCTCCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT  
CACCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG  
TTAAAACTCGGCTTCCCTTTGATTTGCTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC  
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG  
GAGGCGGGTGGCACGCTGCAGCCCGGAGTCCCCGTTACACTGAGGAACGGAGACCTGTGAC  
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAATGCCCCGGG  
GGCAGCAAACCTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA  
GCTGTCAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTTAAATTGTCAAAAA  
GCGCATCTCAGATTCCAGACCCTGCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC  
CTTTCTGAAGGTCGCATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTTT  
TACAGTGAACCTGAAGCTTTAAGTCTCATCCAGCATTTCTAATGCCAGGTTGCTGTAGGGTAAC  
TTTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA  
TTGAGAATGTACTACGGTACTTCCCTCCACACCATAACGATAAAGCAAGACATTTTATAACG  
ATACCAGAGTCACTATGTGGTCCTCCCTGAAATAACGCATTTCGAAATCCATGCAGTGCAGTA  
TATTTTTCTAAGTTTTGGAAAGCAGGTTTTTTTCTTTAAAAAAATTATAGACACGGTTCCT  
AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA  
TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCTATTTTCGC  
ATTTTCAATAAAATGTCTCTAATACAAAAA

## **FIGURE 4**

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF  
TGPMSEDFKNVGLVFNLSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYIINKLHHVDES  
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC  
REPLIPILSLYMGALVRCTTLC LGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL  
ATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN  
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR  
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGVHGATLGVGSL  
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPPTTEEVTDIVEMRENE

### **Transmembrane domains:**

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,  
408-423, 431-445

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## **FIGURE 5**

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT  
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG  
ACAAGAATAACCCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC  
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTCCCTTTGCGGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

## **FIGURE 6**

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG  
GAGCAGGGCAAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC  
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT  
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCCTTTGCGGATTTTCT  
CCTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG  
AAAACCTTTGTCCTTGCCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT  
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCTCCTGGCGGGCA

## **FIGURE 7**

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA  
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT  
CCTACCCTACCTGGGGGTGCACGGTGAGAC

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## FIGURE 8

GCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA  
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG  
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCACGTTCTTCCTCTTCC  
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGAGAGTCAGCTCTACAAGCTG  
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG  
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT  
TCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG  
AATGGGTTTTTGGTTCTTTAAGTTCTTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT  
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCA  
TCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC  
AAGGCCGAGGAGTGCGATTCCCGTGCTGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT  
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGCT  
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT  
GCTGTCCTGCCCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTTCAT  
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG  
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT  
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC  
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTTGGCAGCCTGTGAGGGCCGGGCC  
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT  
GGCCTCACTGCACGTGATGATGACGCTACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA  
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC  
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCT  
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT  
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG  
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA  
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCTGT  
TGCCCATCTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCCTCAGGCTCCACGGGAGCGGGG  
CTGCTGGAGAGAGCGGGGAACCTCCACCCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT  
CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT  
AAGACTTTTTTCTAATAACAAGCCAGTGCGTGTAACAAAAA

## **FIGURE 9**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE  
SPLYKLPWVCEEAGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSW  
NQRWLKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC  
VCVSIAAVLPKVQDAQPNISGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA  
ACEGRAFDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS  
WAGLLLYLWTLVAPLLLRNRDFS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

## **FIGURE 10**

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTG  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA  
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG  
TGA CTGCCGATTCTGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC  
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT  
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAATTGCAGGA  
GCTGTACCGGGAAGTCTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT  
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG  
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAA  
GAGTGGAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC  
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAAACTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC  
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTCTTTTCTTTTCTT  
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA  
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

## **FIGURE 11**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF  
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDVQSAH  
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR  
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE  
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-24

#### **Transmembrane domains:**

amino acids 76-96 and 171-195

#### **N-glycosylation site:**

amino acids 153-156

## **FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTCGTTTCATG  
GCTGGCGCCGAACC

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## **FIGURE 13**

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT  
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGGTGTATGGGGGA  
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA  
TAACC

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## FIGURE 14

GAGCCGCCGCCGCGCGCGCGCGCCGCGCACTGCAGCCCCAGGCCCGGCCCGCCCGCCACCCACGTCT  
GCGTTGCTGCCCCGCCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT  
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTTGCGGGG  
GCTTCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG  
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT  
CGGCGTGGTCATTGCAGTGGGCATCTTCTTGTTCTGATTGCTTTAGTGGGTCTGATTGGAG  
CTGTAAAACATCATCAGGTGTTGCTATTTTTTTTATATGATTATTCTGTTACTTGTATTTATT  
GTTCAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT  
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT  
GTGGGTTCCGAAGTGTTAACCCTAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC  
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG  
TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA  
GGAACCAGAAAGACCCCCGCGCGAATCCTAGTGCAATTCCTTTGATGAGAAAACAAGGAAGAT  
TTCCTTTCGTATTATGATCTTGTTCACTTCTCTGTAATTTCTGTTAAGCTCCATTTGCCAGT  
TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATTGATAGTGGAATTATATATTTTTACT  
CTATGTTTCTCTACATGTTTTTTCTTTCGGTTGCTGAAAAATATTTGAAACTTGTGGTCTC  
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCAATTGTCGGGCACTGTCCACTGTGGCCTT  
TCTTAGCATTTTTACCTGCAGAAAACTTTGTATGGTACCCTGTGTTGGTTATATGGTGAA  
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC  
TGGAAAAAGAGTGGAATTTATTAATAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA  
TCCAAATTCCCAATTTTTTTTTGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA  
TAAAAATGATAATTTACTTGTAGTCTTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT  
GTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT  
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT  
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA  
AAGACTGCATTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGATATTTG  
ATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT  
GTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATTGTGTG  
GCTCTGTATATTCTGTAAATAATTAAGGACAGAAACCTTTCTTTGTGTATGCATGTTTGA  
ATTAAAAGAAAGTAATGGAAG

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## **FIGURE 15**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV  
GLIGAVKHHQVLLFFYMIILLVFIQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQR  
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVFGGIGLFFSFTEILGVWL  
TYRYRNQKDPRANPSAFL

### **Signal Peptide:**

amino acids 1-34

### **Transmembrane domains:**

amino acids 47-63, 72-95 and 162-182

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## **FIGURE 16**

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTC CGAAGTGTTAACC CAAATGACACCTGTNTGGCTAGCTGTGTTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC  
TACAGATACAGGAACCAG

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## **FIGURE 17**

AATCCCAAATTCCCAATTTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG  
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCACTTGC

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## **FIGURE 18**

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

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## FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG  
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTTGAGACGCTGCAGTGTGAGGGACCTGT  
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT  
TCCAGGTCAAGGCCTACACTTTTCAGTGAACCCCTTCACCTGATTGTGTCTTATGACTGGCTG  
ATCCTCCAAGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC  
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC  
TGCAGTGGCATCTTCCAGAGCCCTGGTCCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT  
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG  
CAGGAAGCCCCATGACCCTGAGTTGTGAGACAAAGTTGCCCTGCAGAGGTCAGCTGCCCGC  
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCTACTGGTGTGAGGCAGCCACTGAGG  
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT  
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACCTGCTCCTGA  
GGAGGCCCCCTGGGCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT  
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG  
CAGGATGTGAGAGTCTCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA  
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTTATCCATGATCTCACT  
TAACCACCCCAATAAATCTGATTCTTTATTTTCTTCTTCTTCTGTCCTGCACATATGCATAAGTA  
CTTTTACAAGTTGTCCCAGTGTTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT  
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC  
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA  
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA  
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGT  
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG  
GGCAGTACCCCAACAACGAAAAATAATCTGGCCCAAATGTGAGTTGTACTGAGTTTGAGAAA  
CCCCAGCCTAATGAAACCCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT  
TATCTCTTTCCAGCCTCATTGAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG  
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC  
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC  
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT  
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCG  
ACTCTGTCGTTGCCCTTGATCTTGAACCTTCAGCCTCCAGAACTATGAGAAATAAAATTCTGG  
TTGTTTGTAGCCTAA

09978192.101501

## **FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQAWQDWPLTQVTFYRDGSALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWKQSPQLEIRVQGASSAAPTLLNPAPQKSAAPGTAPEEAPGGLPPPPTPSSDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

**Signal sequence:**

amino acids 1-17

**Leucine zipper pattern sequence:**

amino acids 12-33

**Protein kinase C phosphorylation site:**

amino acids 353-355

09978192-101501



## FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGGGTCCGCCACGCGTCCGGGCCACCAGAAGTT  
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG  
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT  
GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG  
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT  
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG  
CCTGCATGTGAGCCACAAGGTTCAGGAGATGTATCCCTCCAATTGAGCACCCTGGAGATGG  
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG  
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC  
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC  
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC  
AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
TTGAAAGCAACATCTACAGTGAAGCAGTCTTGGGACTGGACCACTGACATGGATGGCTACCT  
TGGAGAGACCAGTGCTGGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT  
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGGAAGACATCCCAA  
CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTTCCATTTTTTGACCCCGT  
CCCTGCCCTCAATTTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC  
AATCCTAAGGCCGGAGGCCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT  
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC  
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA  
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA  
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT  
CCAGTGATGAGCCAACCTTCCCAGAATCTGGGCAACAACACTCTGATGAGCCCTGCATAGGA  
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC  
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCCATTAGGC  
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT  
ACCTCTCTTCCCTGGATAGCCCCAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT  
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG  
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG  
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA  
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT  
TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTTACAGGCCAGGGTTCA  
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA  
ATCATAACAGC

09978192.101501

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHLLTVDTYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKWLVQRGS  
DPVTIFLRDSSGDHIQQAKYQGRHLHVSHKVPGDVSLQLSTLEMDDRSYHTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPISYIWYKQQTNNQE  
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT  
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFTMAYIMLCRKT  
SQQEHVYEAAR

### **Signal Sequence:**

amino acids 1-19

### **Glycosaminoglycan attachment site:**

amino acids 149-152

### **Transmembrane domain:**

amino acids 282-300

09978192-101501

## FIGURE 23

GCGCCGGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT  
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCGGA  
GGCGCCCGGGCCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC  
GGGATGTCCCTCCTCCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA  
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC  
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
AGTGGCCTTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC  
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCAT  
GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATT  
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT  
GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA  
CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT  
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
ATTTTCCTCCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT  
CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAAT  
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC  
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG  
CTAATCTGACCAAAGCAGAAACCACACCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA  
ACGGTCTGAATTACAATGGACTTGACTCCCACGCTTTCTAGGAGTCAGGGTCTTTGGACTC  
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
GTGAGCATTGCACGGAACAGATTGAGATGAGCATTTCCTTATACAATACCAAACAAGCAAA  
AGGATGTAAGCTGATTGATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT  
TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACCTTATTGGATT  
ATTAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
TGAGCTAACCACTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
TTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC  
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT  
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCTCAAAT  
CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT  
TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAGGGATCTAGGAATGCTGAAAGATTA  
CCCAACATACCATATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG  
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDLTLCESSTGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSRSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251

09978192-101501

## FIGURE 25

GTCGTTCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTCGGAGGAGAGCACCCGGA  
GACGCGGGCTGCAGTCGCGGGCGGCTTCTCCCCGCTGGGCGGCCTCGCCGCTGGGCAGGTGCTGAGCGCCCCCTAG  
AGCCTCCCTTGCCGCTCCTCCTCTGCCCCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG  
GCCCGGAGGCGGCGGTGGATGCGGCGCTGGGCAGAAAGCAGCCGCGCATTCAGCTGCCCCGCGCGCCCCGGGCG  
CCCCTGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATC  
GCCCGCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCTTAGCACCACCACAGCTCAG  
CCAGAACAGAAGGCCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT  
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT  
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCATGGCCAATG  
ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCATTTGCCACCTGGCATGTTCCAGTCTAACGCT  
ACCTGTGCCCCCATACGGTGTGTCTGTGGTTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG  
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT  
CTGAGTCAGAACCTGGTGGTGTATCAAGCCGGGGACCAAGGAGACAGACAACGCTGTGGGCACACTCCCGTCTTTC  
TCCAGCTCCACCTCACCTTCCCCCTGGCACAGCCATCTTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT  
TCCTCCACTTATGTTCCCAAAGGCATGAACTCAACAGAATCCAACTCTTCTGCCCTCTGTTAGACCAAAGGTACTG  
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAAGGAAGACGTGAACAAGACCCTC  
CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG  
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCTAGACAGAACCTACACAAG  
CATTTTGACATCAATGAGCATTGTGCCCTGGATGATTGTGCTTTTTCTGCTGCTGGTGTGTTGTGGTGTGTTGTGGT  
TGCAGTATCCGAAAAGCTCGAGGACTCTGAAAAGGGGGCCCCGGCAGGATCCAGTGCCATTGTGGAAGGCA  
GGGCTGAAGAAATCCATGACTCCAACCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT  
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG  
AGGGAGGTGTGCTGCTTTCTCCAATGGGTACACAGCCGACCACGAGCGGGCTACGCAGCTCTGCAGCACTGGACC  
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCCGAGAAACGATGTTGTGGAG  
AAGATTCTGTTGGCTGATGGAAGACACCACCCAGCTGGAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCG  
CTTAGCCCCGAGCCCCATCCCCAGCCCCAACGCGAACTTGAGAATTCGGCTCTCCTGACGGTGGAGCCTTCCCCA  
CAGGACAAGAACAAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC  
TCCGCGCTGAGCAGGAACGGTTCCCTTTATTACCAAGAAAAGAGGACACAGTGTGCGGCAGGTACGCCTGGAC  
CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG  
ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC  
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA  
ATTTAGTGGCAGGGTGGTTTTTTAATTTTCTTCTGTTTCTGATTTTTGTTGTTTGGGGTGTGTGTGTGTGTTTGT  
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTTAAACAGAGAATATGGCCAGTGCTTGAGTTCCTTCTCCTTCTC  
TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAACGTGTTGTGAA  
ATACCCACCACTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTGCTTCTTATGTATTTTCAAGATTATTCTG  
TGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC  
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT  
AAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAAGAAATTTAAGA  
CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTCATATTATGG  
CTGAACTTGACCACACTATTGCTGATTGTATGGTTTTACCTGGACACCGTGTAAGTGCCTGATTACTTGTAC  
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTGCTATTTAAGTGGCTT  
GACAACCTGGGCCACCAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT  
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG  
TTTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGGTGGGATTCTTTCACCAATT  
ACTTTAATTAATAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAAATG  
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTGTGG  
GTAGTGGTGAAGGACGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTTA  
AAAAAAA

09978192.101501

## **FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCSRIARRATATMIAGSLLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLPCA  
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKGTTEDVRCKQCARGTFSDVPSSVMKC  
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQOGPHHRHIL  
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIIVVCSIRK  
SSRTLKKGPRQDPSAIVEKAGLKKSMPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRNDVVEKIRG  
LMEDTTQLETDKLALPMSPSPLSPSPIPSNAKLENSALLTVEPSPQDKNKGFFVDESEPLL  
RCDSTSSGSSALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLFEEIGVKSQEASQTLLDSVYSHLPDLL

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

09978192-104504

## FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGA  
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC  
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTTGGCC  
TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG  
TCACTGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT  
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC  
GAGTACCGCTGTGTCCGGGTGGGTGGTCAAGATGCCGTGCTCCAGGTGTTTACAGCTGCTTC  
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCAAC  
TGGGTTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGAGGTTT  
CGGGAGGAGTTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA  
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCT  
GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAG  
TGGCCCTGGCAGGCCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGGCTCTGTATCAC  
GCCCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA  
CCATCCAGGTGGGTCTAGTTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG  
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA  
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGAC  
GCCTCCCCTGTCTTGAACACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG  
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG  
TGGACAGCTGCCAGGGGGACAGCGGGGGGGCCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG  
TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC  
CCGTGTACCTCCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA  
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCT  
GGAATCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCCGGCACCA  
GTAGCAGGCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTTT  
GTTTTTTGTTTTTTTGGAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA  
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCCTCAGCTTCCCCA  
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAACTAATTTTTTGTATTTTTTAGTAGAGAC  
AGGGTTTCACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT  
CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC  
TGATCTTCACTAAGAACAAGAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT  
CTGGTTTTCTCTCAGGGTCTTGCAAAATTCTTGACGAGATAAGCAGTTATGTGACCTCAG  
TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCAGAAGTGCAGAACTGCAGTC  
ACTGCACGTTTTTCATCTCTAGGGACCAGAACCAACCCACCCTTTCTACTTCCAAGACTTAT  
TTTCACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT  
TGTAGCATTTGGTGCTTGACGTATTATTGTCTTTGATTCCAATAATATGTTTCTTCCCT  
CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

0070492.101501

## FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA  
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVVRVGGQNAVQLQVFTAAS  
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV TALHH  
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT  
PLWIITAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHISKYKPKRLGNDIALMKL  
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPLISNKICNHR  
DVGGGIISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSFSGIGCAEVNKP GVYT  
RVTSFLDWIHEQMERDLKT

### **Signal Peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 240-284

09978192.101501



## FIGURE 29

CCCACGCGTCCGTCCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTCAAGGCTGGCTTGT  
GCCAGAACGGCGCGCGCGCGCACGCACGCACACACGGGGGGGAAACTTTTTTAAAAATGAAAGGCTAGAAGA  
GCTCAGCGGCGGGCGGGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGA  
CGCCCGGCCCGGCTCGGCGCCCCGCTGGGATGGTGACGCTCGCCGCCGGGCCCGAGAGCTGCTGCACTGAAG  
GCCGGCGACGATGGCAGCGCGCCCCGCTGCCGCTGTCCCCCGCCCGCGCCCTCCTGCTCGCCCTGGCCGGTGCTCT  
GCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTGAGTGCCTCTGT  
TCGGAGTGGGGACCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGCTGAATATTGCACT  
ACAACGGGAAAGCAAAGAACTGATCATAAATCTGGAAAGAAATGAAGGTCCTCATTGCCAGCAGTTTCACGGAAAC  
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT  
ACGGGGATATTCTGATTACGAGTCACTGCTCAGCACGCTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAAATGA  
AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAAACTCTTCCAGCGAAGAAGCTGAAAAGCGT  
CCGGGGATCATGTGGATCACATCACAAACACACCAAACTCGCTGCAAGAATGTGTTTCCACCACCCTCTCAGAC  
ATGGGCAAGAAGGCATAAAAGAGAGACCCTCAAGGCACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG  
AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCACGTTGACAA  
GTTTTACAGACCACTGAACATTCCGGATCGTGTTGGTAGGCGTGGAAGTGTTGAATGACATGGACAAATGCTCTGT  
AAGTCAGGACCCATTACACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA  
TGACAATGCGCAGCTTGTGAGTGGGGTTTATTTCCAAGGGACCACCATCGGCATGGCCCAATCATGAGCATGTG  
CACGGCAGACCAGTCTGGGGGAATTGTGATGGACCATTGACACAATCCCCCTGGTGACCGCTGACCCTGGCACA  
TGAGCTGGGGCCACAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA  
AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTTCAGCAGTTGCAGCAGGAAGGACTT  
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTTAACTGCCGGAAGTCAGGGAGTCTTTCCGGGGCCA  
GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG  
CTGCAATGCCACCACCTGTACCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT  
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCCAGAGTTCTGCACAGGGGCCAGCCC  
TCACTGCCCAGCCAATGTGTACCTGCACGATGGGCATCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT  
CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA  
GAGAGTCAATTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCTTTGCCAAATGCGAGAT  
GAGAGATGCTAAATGTGGAATAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC  
CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGGATTCTGTGCCGGGGACCCACGTGTACTTGGGCGATGA  
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA  
AAATATTAGTGTCTTTGGGGTTACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA  
CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCCC  
CATCCGGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG  
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCAGTG  
CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT  
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA  
CAGTGCAAGGAAGGGCAGCGACTTCTGGTTGAGCTTCTGCTAAACATGGACATGCTTCAGTGCTGCTCCTGAG  
AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC  
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCAGTGTCCTTCCCCAGTGACACCTCAGCCT  
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAAT  
AGCAGGGTTTTAGTTTTTAATTTATCAGAGACCTGCCACCCATTCCATCTCCATCCAAGCAAACTGAATGGCAA  
TGAAACAAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC  
AGTACTCAGGTTTGAGGGTTTGCAGAAAGCCAGGGAACCCACAGAGTACCAACCTTCATTTAACAAGTAAGAA  
TGTTAAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCCGTGCCATTACTGCATAAAATAGAGTGCAATTT  
GAAAT

09978192.101501

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGDLWIPVKSFDSK  
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCCYYHGHVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDKF  
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFNMHDTLDRGCSCQMAVEK  
GGCIMNASTGYPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFQQKCGNRFVEEGEE  
CDCGEPEECMNRCNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS  
PHCPANVYLHDGHSCQDVGDCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN  
CGKVSXSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG  
DDMPDPGLVLAGTKCADGKICLNRCQNIQSVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP  
FCDKFGFGGSTDSGPQRQAERQEAESNRERGQGEVPGSQEHASTASLTLI

**Signal peptide:**

amino acids 1-28

## FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTTCCCTGACAACGAAA  
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANNTTCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCCTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCCAGTGTCCTTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

09978192.101501

## FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA  
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCCTCGGCCTCCC  
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTAAAGAAGTTAAT  
GAAACCATACCTTTTACATTTTAAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAAA  
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA  
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA  
CTTTTAACAAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG  
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTTCGAAATCTGCCT  
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA  
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC  
TTGAATATAAGACCCTACTTGCTATCTCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC  
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGGTAAGGGGATGGTGGCGA  
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT  
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCT  
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG  
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAACCGAATCCAATGGTGCCT  
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT  
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT  
GACTAGATGATAAATGCCTGTACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG  
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA  
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG  
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA  
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAGTGGCT  
CACGCCTGTAATCCCGGCCTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA  
AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGG  
GATGGTGGCAGGCACCTGGAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA  
CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG  
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL  
LHLYH

**Signal peptide:**

amino acids 15-27

09978492.101501

## FIGURE 34

GCCGCGGCGAGAGCGCGCCAGCCCCGCGCGATGCCCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCCGGC  
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGGGCGGCGCTGGGGCGCCCGGGCCAGG  
AGGCGGCGGCGGCGGCGGCGGACGGGCCCCCGCGGCGAGCGGCGAGGACGGACAGGACCCGACAGCAAGCACC  
TGACACGGCCGACATGTTACGACACGGGATCCAGAGCGCCGCGCACTTCGTCAATGTTCTTCGCGCCCTGGTGTG  
GACACTGCCAGCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT  
ATGTGGCTAAAGTGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGCGAGGATACCCACCTTAA  
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCGGGACTTCAGACACTGGAAAACTGGATGC  
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGAACCGCCAGTGCCCCGAGCTCAAGCAAG  
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC  
CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCGAAACTG  
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTGCTCCGGAAACCAGGTTCTGGCTATCCCCTC  
TTCTCTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGAAAGCGGGATTTGGAGTCACTGAGGGAGTACG  
TGGAGTCGACGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCCGGTGTGGCAG  
CTGAGCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAA  
TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCACTGTAAGACTCTGGCTCCTACTTGGGAGGAACTCTCTA  
AAAAGGAATTCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA  
AGTATTCGGTACGAGGCTACCCACGTTATTGCTTTTCCGAGGAGGGAAGAAAGTCACTGAGCACAGTGGAGGCA  
GAGACCTTGACTCGTTACACCGCTTTGCTCTGAGCCAAAGCGAAAGACGAACTTTAGGAACACAGTTGGAGGTAC  
CTCTCCTGCCAGCTCCCGCACCCCTGCGTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTTCCCAGTGGTGGCT  
GTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTTTCCAAGCCAAACACACTCTACAG  
ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAAACATTTTTCAGTGGCGATA  
TATCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA  
TTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC  
CCACGAGTTCTGGAAAGGTGGCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTCACAGTTGACTCAATAC  
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC  
TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC  
GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTGATACTTGTCAAATCAGTTACTGTTCAAGGGAT  
CCTTCTGTTTCTCACGGGGTGAAACATGTCTTTAGTTTCTCATGTTAACACGAAGCCAGAGCCACATGAACGTG  
TGGATGTCTTCTTAGAAAGGTTAGGCATGGAAAATCCACGAGGCTCATTTCTAGTATCTCATTAACCTATTGA  
AAGATTCCAGTTGTATTTGTACCTGGGGTGACAAGACCAGACAGGCTTTCCAGGCCCTGGGTATCCAGGGAGGC  
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAGAGG  
CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC  
CAAAGACAGATGTGAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA  
ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA  
GATAGGTGTTGTCTTTTACCATCGAGCTACTTCCATAATAACCACTTTGCATCCAACACTCTTACCCACCT  
CCCATAACGCAAGGGGATGTGGATACCTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCATTATA  
CTGTCTGTCTGAGGCAGAAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCACG  
TATGGTTACAGATAATCTTTTTTTTAAAAAAACCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA  
CACAACTTCAGCTTTCATCACGAGTCTTGATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTTACACTAT  
GATACTTTCTAAATAAACTCTTTTTTTTTTAA

09976192-101501

## **FIGURE 35**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS  
KHLTYADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNMEDAKVYVAKVDCTAH  
SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPE  
LKQGLYELSASNFEHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT  
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA  
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA  
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDLHRLFVLSQAKDEL

**Signal sequence:**

amino acids 1-32

09978192.101501

## **FIGURE 36**

CTTTTCTGAGGAACCAACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA  
CCGCTGAAGTCTGTGCCACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG  
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCACACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT  
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAAAAAA



## FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEGEG  
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGCRY  
RKFBVGQLDISIARLKTSMKFVKNVIAGIRETEEFYIVQEEKNYRESLTHCRIRGGMLAMP  
KDEAANTLIADYVAKSGFFRVFIGVNDLREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC  
VEMLSGRWNDTECHLTMYFVCEFIKKKK

**Signal peptide:**

amino acids 1-25

09978192.101501  
TOSTOT.26T87660

## FIGURE 38

GGTTCTATCGATTTCGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGCCTGGGTGGGAATCGGCGTGT  
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT  
CGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC  
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA  
AGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT  
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG  
TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACCTGGCCCAGCAGCGCGCCGCGC  
ACACCTTTCTCATTACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC  
AGGGCTGCACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAG  
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG  
GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT  
CTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG  
GTTCCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC  
CCCTGCTGCACTGCCTCCGCAGCTGCGGCGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG  
GAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG  
CCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
GGCCAGTGCCAGGATACTCTCTTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC  
ACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG  
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCAC  
TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG  
GTGCTGAAATCCAAGTTCTCGGCTGGTCACTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC  
GGTGTTCCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCCGAGCAAGGCAG  
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGT  
TTTGTGCGGCGCTTCCGGGCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT  
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC  
ATATCTTCCCCTTCTCCTTGATTGCTATGATGTCAACCAGGAGAGCCAATTCGGGACCCC  
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCCGTAAGCCA  
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG  
ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA  
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC  
CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG  
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC  
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG  
GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG  
TTCGGATGGCAAATGAGGGCTTCGACCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC  
CAGGCTGTAGGTGCCTACCTGCCCTCACAACTGCCCGGTACAGCGCCCTCCTGGCAGGAAA  
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGG  
CCGTTGCAGGTGTACTGGGCTGTGAGGGATCTTTTCTATAACCAGAACTGCGGTCACTATTTT  
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC  
TTGGCCGCCATGGCCCAACTTGTTTATTGCAG

## **FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913

><subunit 1 of 1, 730 aa, 1 stop

><MW: 78644, pI: 7.65, NX(S/T): 2

MGVCQRTAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLPLLLLLPL  
LLLKLHLWPQLRWLPADLAFVRLCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ  
RAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGVPVGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP  
SKAERGHKVRRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFSLIRYDVTTGPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPPELAQ GK  
LLKDVFVRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK  
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

**Type II transmembrane domain:**

amino acids 45-65

**Other transmembrane domain:**

amino acids 379-398

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at amino acid 136

**CUB domain protein motif**

amino acids 254-261

**putative AMP-binding domain signature**

amino acids 332-343

**N-glycosylation sites**

amino acids 37-40 and 483-486

09978192.101501

## FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA  
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC  
GCTTGTCCATCTCCCTCCCGGGGGAGCCGGCGCGCTCCCACCTTTGCCGCACACTCCGGC  
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC  
CCATGGTGGTTTTTTTAAACACTTCTTTTCCTTCTCTTCCCTCGTTTTGATTGCACCGTTTCCA  
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCAGCCAGCCCTTGTTGGCTTGCCATCGT  
CCATCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCCTCGG  
CTGGCAGAAGGGGGTGACGCTGGGCAGCGCGCAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT  
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTTGTATG  
TTGCACCAATGCCCTTCTTGATCGGGGCTGTGATTCTTCCCTCTTGGGGCTGCTGCTCTCCC  
TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC  
AAGGGATTACGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG  
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC  
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG  
CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA  
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT  
TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC  
TTTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCTCAGTATCACTTCAGTGA  
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC  
GGAAACTGAAGATTACAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG  
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCAGGGTGTATCCG  
TGCCCTCATGAAGATGCTGTACTGCCCATACTGTGCGGGGCTTCCCACTGTGAGGCCCTGCA  
ACAATACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG  
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGGCCATTCAACAT  
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA  
ACAGCATGCAGGTGTCTGCAAAGGTCTTTTCAAGGATGTGGTCAGCCCAAACCTGCTCCAGCC  
CTCAGATCTGCCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTCAAGCCCTACAATCCTGA  
GGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA  
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC  
GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT  
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA  
TCACTCGGCCTGACACTTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA  
CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG  
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCCACGGAGTTTGAGTTTGTACCA  
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC  
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTTGGCACTGCAGAGACTGTGCAGATA  
ATCTTGGGTTTTTTGGTCAGATGAACTGCATTTTAGCTATCTGAATGGCCAACCTCACTTCTT  
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCGTTTTCTATGAGAAGAGAG  
CAGTAATGCAATCTGCCTCCCTTTTTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG  
CTTCCTCTTTCCTTCAGCTATCTGTGGGGACCTTGTTTTATTCTAGAGAGAATTCTTACTCAA  
ATTTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAAT  
CTCACGTTGTGAGGGTTTTTTTTTTCTCATTTAAAT

## **FIGURE 41**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADV KARS CGEVRQAYGAKGFSLADIPYQEIAGEHLRICPQ  
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF  
VRTYGMLYMQNSEVFQDLFTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY  
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL  
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES  
VMDPIDVKISEAIMNMQENSMQVS AKVFQGCQPKPAPALRSARSAPENFNTRFRPYNPEER  
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE  
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG  
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

**Signal peptide:**

amino acids 1-23

09978192-101501

## FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG  
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG  
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT  
GGAGGGAGATCAGGAAACGGCTTCTTCCTCACTTCGCCGCTGGTGAGTGTGCGGGGAGATTGGCAAACGCCTAGG  
AAAGGACTGGGGAAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG  
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA  
TCCCCGCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCCAACGTGAGGGCGCTCTGGCCACGA  
AAAGTTCTGTCCACTGTGATTCTCAATTCCTTGCTTGGTTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA  
ACTTTTTTCTTTTTTTTTTTTCTTGGTGGAAGCTGCTCTAGGGAGGGGGAGGAGGAGGAGAAAGTGAAATGTGC  
TGGAGAAGAGCGAGCCCTCCTTGTTCTTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT  
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCACCGTCTGTTGGGTGCATG  
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA  
GGGGCTGTGCGGGGCATCCGCCCTCCGCCTTCTCCACAGGCCTGTGTCTGTCTGGAAGATGCTAGCAATGGGGG  
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGCGGGCCAGGCCTTAGAAGAGGAGG  
AAGAAGGGGCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCCAGCACAACTTCCACCTCCAGCCCCATCTCA  
TTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTTACCACGGATCTGAGATTAAACACCTACTCTTG  
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT  
TTATTACTGGAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCCAACTGTTTAC  
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTCGGAAAATGGCACT  
TGGGTTTTTAACAGAAAAGAATGCATGCCACCAGAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG  
GGGATTACTATACACTACAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG  
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCATA  
ACCCACAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTCACTTACCAGTGAAGCTCCTGGCAGGTATT  
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAAGATATGCTGCCATGCTTTCCTGCTTAGATGAAGCAA  
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG  
GTGGCCAGCCTACGGCAGGAGGGAGTAAGTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC  
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACTTGTGCACATCACTG  
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT  
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGCATAACATTGACCCCTATACACCAAGGC  
AAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG  
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG  
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA  
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAC  
TGCAGTGCCGGTCAGGTATCCCCCAAAGACCCAGAAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG  
GTATAAAGAGGAAACCAAGAAAAAGAAGCCAAGCAAAAATCAGGCTGAGAAAAAGCAAAAGAAAAGCAAAAAAA  
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA  
GGCTTGTTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCCACTGAAAACGTCTCTGCTCAGTG  
CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG  
GTGAGTCTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAACTGCTTTGAATTATAGGAGGAGAAACAATA  
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC

## **FIGURE 42B**

AGTCAAAGATTGTGTCACCTCAAAGGCCTTGAAGAATATATTTTCTTGGTGAATTTTTGTATGTCTGTGCATATGA  
CACTTGGGTTTTTTAATTAAATTCTATTTTATATATATAAATATATGTTTCTTTTCCTGTGAAAAGCTGTTTTTCT  
CACATGTGAACAGCTTGACACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC  
ACAATGAATGTAACATTTTTCTAAACACTTTACTAGAAGAACATTTCAGTATAAAAAACCTAATTTATTTTACA  
GAAAAATATTTGTTGTTTTTATAAAAAGTTATGCAAATGACTTTTTATTTTATTTCCCTGCATACCATTAGAAGA  
ATTTTATTTCAATTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA  
TAAAAAACATCATTCAGAAAACTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT  
ATTACTTGGAAATCAATGTTTGTGTCAGAGTTGAGACAACCTTTATTTGTTTCTATCATAAACTATTTATGTATCTT  
AATTATTAAAAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAATT  
GTATCATTTGGTCCTAAAAAATAAAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACAACCACAGTAA  
TATAATATGATTTTACAGATAGATGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCCATAATAATAACTAA  
TATTTATATTAGGTTGGTGCAAAACTAGTTGCGGTTTTTCCCATTAAAAGTAATAACCTTACTCTTATACAAAGT  
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGAAACCCC  
ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA  
GATTGGTGTGGATCCTGTAGACCCTGGTGTTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTAC  
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT  
GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC  
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT  
CTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGATTTTAATTTTAACATTTTATTTCTAGAATATAT  
GGCTCCATTTTATTTTATAGTGTAAGTTGATTTTCTAAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAG  
TCTTAAAAATAAAGGCATATTGTTTATGTTTTAA  
AA

0978192-101501

## **FIGURE 43**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAGVKLENYYVQPICTP  
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVKGWHLGFNRKEC  
MPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCYDLYENDNAAWDYDNGIYSTQMYTQRVQQ  
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA  
LKTYGFYNNNSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVFVHSPLLKNKGTVCK  
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG  
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS  
TSQPTHMRGWTYLTGIQES

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-37

#### **Sulfatases signature 1.**

amino acids 120-132

#### **Sulfatases signature 2.**

amino acids 168-177

#### **Tyrosine kinase phosphorylation site.**

amino acids 163-169

#### **N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321

09978192-101501



## FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC  
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGCTCAGGAGGAGGAAGGAGGAC  
CCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG  
GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCT  
GGGGTCTGTCACTATGGAATAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG  
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAAT  
GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG  
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT  
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTTAGGACATGTGCCATGATAA  
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA  
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAATGTACACA  
TTGGTTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT  
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCTTCAAGTG  
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG  
TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC  
AAAAACAGCATGAAAAAGAAGGCCAAAAATTAAAAATGTTACCCAGAACCCACCAGGACTCC  
TACCCCTAAGGTGAACCTTGCAAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAC  
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAAGAGGGGCTTGAGGATGAGAAAAGAG  
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT  
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA  
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT  
GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC  
TTCTATATGGCAGTTCCGGCCTTGGCAGGTCACAAGAAAGACATTGGCCGATTGAAACTTCT  
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG  
ACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG  
ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAAATTGAGTTGTATCAAGGAACTGATGC  
TACCAAAGCATCATTTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCGAAATCGCAGTGG  
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG  
TTACTATCTTTATATTTGACTTTGTATGTCAGTTCCCTGGTTTTTTTTGATATTGCATCATAG  
GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG  
TAAGATGCCTTTCTTGATATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT  
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC  
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA  
GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGA  
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC  
TTGTATATTTAATTCTTTGTAATAATAA

## **FIGURE 45**

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE  
ATCEPGCKFGECVGPNNKRCRCPGYTGKTCSQDVNECGMKPRPCQHRVCNTHGSYKCFCLSGH  
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP  
YNRRVCNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPPK  
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

**Signal peptide:**

amino acids 1-21

**EGF-like domain cysteine pattern signature.**

amino acids 80-91

**Calcium-binding EGF-like domains**

amino acids 103-124, 230-251 and 185-206

## **FIGURE 46**

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG  
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC  
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGCTGCTGTCAGCCAGAAGAGTGCAT  
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT  
TGTTTTGCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCAGCGTTCTCTGTGC  
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC  
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTCCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC  
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC  
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTAAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAAAAAG  
ATTGCCATGAATCTTGCAAAA

09978492-104504

## **FIGURE 47**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343

><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL  
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP  
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSCVRLMLISMANDLKEVWISEQPFLLVTYLW  
QYMPTWAWWITNKMGGKKRIENFKSGVDADSSYFKIFKTKHD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 136-157

#### **Tyrosine kinase phosphorylation site.**

106-113 and 107-114

#### **Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

## FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCGG  
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC  
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTC  
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT  
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCCAAGGCAAGGCTAAGAGGCACTGAGCCCTCA  
ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG  
GACAGCGTGGCCCCGGCCCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC  
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
CTGGGTCTCTACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT  
CAGTGGTCTCTGGGTTCTCTGCAGCGTGAAGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG  
GCTGCCCTGCAGTTGCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
GCAGCTCGCCACCCACAGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC  
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC  
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGTATCTACAACCAGCT  
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGGCCCCCAGCCTG  
GGGTGCAGGGCCCCCTGTGAGGAGATTCCGGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA  
CACTGGGTTTCAAGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT  
GCTGCTGACCAACACAGCTGCTCACAGTTTCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT  
TCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCCATGGCCCTGGGAGGCCAGGCT  
GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG  
CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA  
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG  
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC  
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTGGGACGG  
GCCCCCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG  
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG  
TGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGGTG  
CATGAGGTGAGGGGCACATGGTTTCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG  
CCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG  
ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC  
AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
AGGCAGGCAAATGGCATTACTGCCCCCTGTCTCCCCACCCTGTCATGTGTGATTCCAGGCAC  
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA  
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGCTACCAAGC  
AGGCGTCTCAGCTTTCCTCCTCCTTTACTCTTTCAGATACAATCACGCCAGCCACGTTGTTT  
TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTAACTTAAATAAATTGTTAC  
AAAATAAAA

## **FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV  
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARGMLCGGPQPGVQGPCQGDSGGPVLC  
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQGLACGGALVSEEAVLTAAHCFIGRQAPEEWSV  
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG  
WVLGRARPGAGISSLQTVPVTLGPRACSRSLHAAPGGDGSPILPGMVCTSAVGELPSCEGLS  
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP  
GSCLANISQPTSC

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

#### **N-glycosylation sites.**

amino acids 37-40 and 564-567

#### **Kringle domains**

amino acids 79-96, 343-360 and 235-247

## FIGURE 50

CGGGCCGCCCCGGCCCCCATTCGGGCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAG  
CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT  
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG  
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC  
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA  
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGAGCCT  
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTGAGCCT  
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT  
TGGCAGGATGGGCAGGGTGTGCCCCTGACTGGCAACGTGACCACGTGCGCAGATGGCCAACGA  
GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGTGCTGGGTGCGAATGGCACCTACA  
GCTGCCTGGTGCACCAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCACCATCACAGGG  
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT  
TGCACTGCTGGTGGCCCTGGCTTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG  
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC  
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCAAAGGATGCGATACAC  
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT  
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT  
GCCTTATTTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC  
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTTCTCCAAAGATGCAATATTGAGA  
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTACCCCGGCCTTGTTTC  
TCCAATGGCCGTGATACACTAGTGATCATGTTGAGCCCTGCTTCCACCTGCATAGAATCTTT  
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCTTTT  
CCCTCCTTCCCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG  
AGGGGACTGCCCCCACCCTCATGGTGTCTATTCTGGGGCTGGGGCAGTCTTTTCTTCTGGC  
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG  
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC  
TCGGAGGGATTTTGTAAACTGGGGGTATATTTTGGGGAAATAAATGTCTTTGTAAAAAAA  
AAAAAAA

## **FIGURE 51**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ  
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASRLRLQVRVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDGQGVPL  
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEKSKTALQPLKHSDSKED  
DGQEIA

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 251-270

#### **N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

#### **Homologous region to Immunoglobulins and MHC**

amino acids 217-234

09978192-101501



## FIGURE 52

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC  
CTGAACTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG  
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCCCTTGCTTCAGCAACATGAGGCTTTTCT  
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACCTTCTTTGATTGGGGCTTTGATCCCTGAACCA  
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAAGGAGGGGA  
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC  
ACAAACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT  
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGC  
TCTGGGCTATGGAAAAGAAGGAAAAGGTAAAATTCCTCCAGAAAGTACACTGATATTTAATA  
TTGATCTCCTGGAGATTTCGAAATGGACCAAGATCCCATGAATCATTCGAAGAAATGGATCTT  
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA  
ACATGGTGCAGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAAG  
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
TAGAGATACATCTACCCTTTTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA  
AGAACATTTTATTTTATACAAATGTTCTTTCTTGCTTTGTTTTTATTTTTATATATTTTTT  
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT  
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTTACAG  
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC  
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTC  
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGAATAGCCCAAGGCTTGCTATTTTTCAT  
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA  
TGGTTGTTGGACCTGACTTGTAAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG  
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG  
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA  
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGTGATGCGTGCCTGTAATCCCAGCT  
ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAACCCGAGGCGGAGGTTGCGGTAAGCCGAG  
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAGAAAAGAACACGGTTAATACCATATNA  
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT  
TGGTGGCCTATTATGATAAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG  
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC  
TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA  
TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTTCTGTCTCATCAAAAAC  
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG  
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA  
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG  
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC  
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA  
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

## **FIGURE 53**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194

><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL  
FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST  
LIFNIDLLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED  
IFDKEDDKDGFISAREFTYKHDEL

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

09978492-101501

## FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT  
CCAACCATTCCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCCAACCGA  
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT  
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC  
CTGCCACCCTCAACGTCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGC  
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC  
TGAGGAGATGTTCCCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG  
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTTCGGTGATGCTGAGAAACGTG  
CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGG  
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
CCGTGATTGTGGGTGCCTCCGTGGGGGCTTCTGGCTGTGGTTCATCTTGGTGCTGATGGTG  
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC  
CTGCAGCCTCCCGTGTCCCGTCTCTCCCTCTCCGCCCTGTACAGTGACCTGCCTGCTCG  
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAACCCCCG  
ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA  
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG  
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA  
GGAGGGGCCGCTGTACCTGCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG  
GGAGGGAGGGCTTTCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCTGGCACGGCTG  
TGCTCTCCCTGCTCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA  
AACTTGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG  
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT  
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC  
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG  
GCTCTGCCTTCTCCATGGGGTAACCACCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT  
GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTT  
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG  
GCATAAGGGGAGGCCTTGGAACTGAGCTGCCAATGCCAGCCCTGTCCATCTGCGGCCACG  
CTACTCGCTCCTCTCCCAACAACCTCCCTTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC  
ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT  
CTGTTTGTAGTAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG  
GTGGCGTGTGCCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAAGCCG  
GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC  
ATAGAGAGACTCCATCTCAAAAAA

09978192.101501

## **FIGURE 55**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI  
YNCYIMNPPDRHRGHGKIHQLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK  
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 161-179

#### **Immunoglobulin-like fold:**

amino acids 83-127

#### **N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

09978192-101501  
TOSTOT-26T8/660

## **FIGURE 56**

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC  
TCAATGGCTCTGACGCCCCGCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCCCTCCAG  
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCCAAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAACCTGCTACATCATGAACCCCCC

09978192-101501

## **FIGURE 57**

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC  
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG  
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTTCGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

# FIGURE 58

TCGGGCGACCGTCGTACACCATGCGGCCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT  
 TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGGACGTACCCCCCAGTGGTGCTGGTCC  
 CTGGTGATTTGGGTAAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA  
 CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAAGTGTGCTGCTGCCTGTATCATTTGACTGCTGGATTGACAATA  
 TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG  
 GGAAGACCTTCTCACTGGAGTTCTTGGACCCCAAGCAAGCAGCGTGGGTTCTATTTCCACACCATGGTGGAGA  
 GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG  
 AAAACGGGCCCTACTTCTTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGGCCCCGTGGTGC  
 TGGTTGCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCGAGCGGCAGCCGAGGCTGGAAGGACAAGT  
 ATATCCGGGCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAGACCCTGCGCGTCTGGCTTCAGGAG  
 ACAACAACCGGATCCCAGTCATCGGGCCCTGAAGATCCGGGAGCAGCAGCGGTGAGTGTCTCCACCAGCTGGC  
 TGCTGCCCTACAATAACATGATGCTCACCTGAGAAGGTGTTTCGTGCAGACACCCACAATCAACTACACACTGCGGG  
 ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG  
 AAGCCACGATGCCACCTGGCGTGCAGCTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACT  
 ATGAGAGCTTCCCTGACCGTGACCCATAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACTTGAAGAGTGCCC  
 TGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACAAGTGTGTGCTGCAGGAGCTGCCAGGCAGCGAGCACATCG  
 AGATCTGGCCAACGCCACCAACCTGGCCTATCTGAAACGTGTGCTCCTTGGGCCCTGACTCCTGTGCCCACAGGA  
 CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCCCTCTGGGGCTGTATGGGCCACGCGTTTTCGCAAGTTTGTGA  
 CTCACCATTCAAGGCCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCCTTTCTCT  
 GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGGGA  
 ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTGGTCCCAGTCCCTGCGCTGGGGCCATG  
 TGTCCCCCTATTCTGTGGGCTTTTCATACCTTGCCCTACTGGGCCCTGGCCCCGAGCCTTCCCTATGAGGGATGTT  
 ACTGGGCTGTGGTCCCTGTACCCAGAGGTCCCAGGGATCGGCTCCTGGGCCCTCGGGTGACCTTCCCACACACCA  
 GCCACAGATAGGCCTGCCACTGGTCATGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC  
 TGACTGGCTTCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGAGTTTGTGCGTTCTTCGTGGTTCCCAGGC  
 CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG  
 CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC  
 CTCCCTTCAACCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTGGAGCCATGGCCTTCTGGGAACCTATGGA  
 GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCACCATCA  
 CACTGCCACCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTGAGCACAGGGCTGAGGATGGGGCTCCTATCCAC  
 CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCAGAACTTGAATGGGACCCTGAGAGAGCCAGGGGTCCCC  
 TGAGGGCCCCCTAGGGGCTTTCTGTCTGCCCCAGGGTGTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT  
 CAGGGCTGCCTTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGT  
 GGGGTTCCCAAAGACGCCTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCAGCTGGATTTTCTCTG  
 TTGCATACATGCCTGGCATCTGTCTCCCTTGTCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG  
 GATTCTGGCAATAAAGTACTCTGGATGCTGTAAAAA

0978192-101501

## **FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH  
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDVRVPGFGKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ  
LYGGPVVLVAHSMGMNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI  
PVIGPLKIREQQRSAVSTSWLLPYNITWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWL  
MQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLLGP

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Potential lipid substrate binding site:**

amino acids 147-164

#### **N-glycosylation sites.**

amino acids 99-102, 273-276, 289-292 and 398-401

#### **Lipases, serine proteins**

amino acids 189-201

#### **Beta-transducin family Trp-Asp repeat**

amino acids 353-365



## **FIGURE 60**

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGG  
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA  
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG  
AGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT  
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT  
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTCACCAAC  
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT  
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAA  
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAAGTGCCA  
GCCCTCTCTTTACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA  
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGGCCCCGGTTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG  
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCA  
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT  
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG  
CTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCAGACTCTGTC  
TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG  
GAATAAATGTTTTCTCATTCAAAG

0978192 101501

## **FIGURE 61**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGE GYSNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVI GDLLFSALWTFWLVGFC  
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

### **Important features:**

#### **Type II Transmembrane domain:**

amino acids 1-45

#### **Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

#### **N-glycosylation site.**

amino acids 97-100

09978192-101501

## FIGURE 62

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG  
CCCGTGGCCGAGGCCCCCCAGGTGGCTGGCGGGCAGGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG  
ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCCGGGCTACCTCCGCCTGGTGCCCTGTTTGTGCTGCTG  
GCCCTGCTCGTGCTGGCTTCGGCGGGGGTGCTACTCTGGTATTTCTAGGGTACAAGGCGGAGGTGATGGTCAGC  
CAGGTGTACTCAGGCAGTCTGCGTGCTACTCAATCGCCACTTCTCCAGGATCTTACCCGCCGGGAATCTAGTGCC  
TTCCGCAGTGAAAACCGCCAAAGCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCCTGGGAACCTTACTAC  
AACTCCAGTCCGCTCTATTCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTCAATTCTCCAAATCCCCGAG  
CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGACGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC  
TCGGCTGCCGTCCCCCTACAGGGCCGAGTACGAAGTGACCCCCGAGGGCCCTAGTGATCCTGGAAGCCAGTGTGAAA  
GACATAGCTGCATTGAATTCCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCCGGCTG  
AAGGGCCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACCTCCGG  
CTGGAGTGAGCGCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCCCTGGAGAAGAGGCTC  
ATCACCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTCGGGGGCCATCATGGCGGTC  
GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGT  
GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCCAGGGCGTCCCTCAGCACCCCGTACTTCCCCAGCTACTAC  
TCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGTATGCC  
TATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAGGGCCAGTGACGATCCAGAACAGGAGGCTGTGT  
GGCTTGCGCATCCTGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACC  
TCCAGATCTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACAGTCGGACCCCTGCCCTGGA  
GAGTTCCTCTGTCTGTGTAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCAACGGCCTGGAT  
GAGAGAAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGACAGCACATGCATCTCACTGCCCAAGGTCTGT  
GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCAAC  
TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCGACTGCAGGGACGGC  
TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGTCTCCGAG  
GGTGAGTGCCCATGGCAGGCCAGCCTCCAGGTTCCGGGTGCACACATCTGTGGGGGGGCCCTCATCGCTGACCGC  
TGGGTGATAACAGCTGCCCCACTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGCTGTGGACCGTGTTCTGGGC  
AAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCAC  
GAAGAGGACAGCCATGACTACGACGTGGCGCTGCTGCAGCTCGACACCCGGTGGTGCGCTCGGCCGCGCTGCGC  
CCCGTCTGCTGCCCCGCGCGCTCCCACTTCTTCGAGCCCCGGCTGCACTGCTGGATTACGGGCTGGGGCGCCTTG  
CGCGAGGGCGGGCCCCATCAGCAACGCTCTGCAGAAAGTGATGTGCAGTTGATCCACAGGACCTGTGCAGCGAG  
GCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGCTACCGCAAGGGCAAGAAGGATGCCTGTCAAGGT  
GACTCAGGTGGTCCGCTGGTGTGCAAGGCACTCAGTGGCCGCTGGTTCCCTGGCGGGGCTGGTCAGCTGGGGCCTG  
GGCTGTGGCCGGCCTAACTACTTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG  
ACCTGAGGAAGTGGCCCCCTGCAAAGCAGGGCCCCACCTCCTGGACTCAGAGAGCCCAGGGCAACTGCCAAGCAGG  
GGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTCGTCC  
CTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCCTGAGGACC  
CAGGCCCCACCCAGCCCTTCTGCCTCCCAATTCTCTCTCCTCCGTCCCCTTCCCTCCACTGCTGCCTAATGCAAG  
GCAGTGGCTCAGCAGCAAGAATGCTGGTTCTACATCCCAGGAGTGCTGAGGTGCGCCCCACTCTGTACAGAGG  
CTGTTTGGGCAGCCTTGCCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCCCTGGTCTAACTTGGGATCTGGGAAT  
GGAAGGTGCTCCCATCGGAGGGGACCCCTCAGAGCCCTGGAGACTGCCAGGTGGGCCCTGCTGCCACTGTAAGCCAA  
AAGGTGGGGAAGTCTGACTCCAGGGTCCTTGCCCCACCCCTGCCTGCCACCTGGGCCCTCACAGCCCAGACCCCT  
CACTGGGAGGTGAGCTCAGCTGCCCTTTGGAATAAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 63**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152

><subunit 1 of 1, 802 aa, 1 stop

><MW: 88846, pI: 6.41, NX(S/T): 7

MPVAEAPQVAGGQGDGGDGEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT  
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGQVLRLKGPDHLASSCLWHLQGPKDLML  
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFAQACEVNLTLDNRLDSQGVLSPTYFSPSYSPQTHCSWHLTVPSLDYGLAL  
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS  
LPKVCDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDGRDGSDEEHCD  
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAACHCFQEDSMASVTL  
WTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA  
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG  
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 46-67

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 604-609

#### **N-glycosylation sites.**

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512

#### **Kringle domains.**

amino acids 746-758 and 592-609

#### **Homologous region to Kallikrein Light Chain:**

amino acids 568-779

#### **Homologous region to Low-density lipoprotein receptor:**

amino acids 451-567

## **FIGURE 64**

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT  
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACCTATGGCTTGTACAACCAAGTCGGACCCCTGCC  
CTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA  
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG  
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTTCGGGGTCGACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCGTGTTCTTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT  
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCCGCGTGCGCC  
CGTCTGCCTGCCCCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG  
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGACTCAGGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCACTGGGGCCTGGGCTGTGGCCGG  
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCCACCTCCTGGACTCAGAGAGCCCAGGGC  
AACTGCCAAGCAGGGGGACAAGTAT

09978192 : 101501

## FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG  
CTCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCG  
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTTGTTTTTTAAA  
ACTTCTGTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCTCTGCTCTG  
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC  
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG  
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCCGCCACAG  
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACGGAT  
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTGAGCCCTGCACACAAGA  
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA  
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG  
AGAAGGACGATTTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG  
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC  
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG  
TGGATGTCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTCAGATGCCTGTG  
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT  
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG  
TCCACCTCTTTGTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTTGCCTTCCAGTGCCT  
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT  
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG  
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA  
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA  
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT  
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

0978192.101501

## **FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDPEHE  
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWL  
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV  
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS  
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:**

**Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

09978192-101501

## FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCGCTGGGCAAGGGCCGGGGCGCCGGGGCCGAGCCACCTCTTCCCCCTCCCCCGC  
TTCCCTGTGCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGGCTGACAGT  
CGGCAAAGTTTGGCCCCGAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACCAGGCCAGACCAGGGGGCGCTCG  
CTGCCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTACAGGAGCCGGCCCCCGGGAG  
AGAAGAGTGCGGCGGGCGGACGGAGAAAAACAACCTCCAAAGTTGGCGAAAGGCACCGCCCTACTCCCGGGCTGCCG  
CCGCTCCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG  
CACCAGGGAGCCTGGGCGCCCGGGCTCCGCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTTCCG  
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCCCTCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG  
ACCGGATTATTTTTCCAAATCATGCTTGTGAGGACCCCCCAGCAGTGCTCTTAGAAGTGAGGGACCTTACAGA  
GGCCCCCTGGTCCGGGACAGCCGCACCTCCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG  
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCTACGCTCCCCTCTCCAGCCAC  
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCGGGGCAACGTACCATCACTTACAGCTATG  
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG  
AGTTTCAGTGCCCTGAACACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT  
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGCTCCCTCCTGCTTGAATG  
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT  
CCTGCCATTGGCTGCTGGACCCCATGATGGCCGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTGG  
GAGATGCAGTGATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTACCCACTTCA  
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTTACCACACAGTTGCTTGGAGCA  
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGGCTTGGGACAGACCCTGTGGCTTAGGCT  
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT  
GTGCTGACGGCACAGATGAGGAGGACTGCCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCT  
CTGGTGCCACAGCCTGCTACCTGCCTGCTGACCGCTGCAACTACAGACTTTCTGTGCTGATGGAGCAGATGAGA  
GACGCTGTCCGCAATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG  
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTATTACAG  
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA  
TTCGCACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC  
CTTCTACGGGCAGCTCATTTGCCAGGGTGCCATCCCACCTGTAGAAGACTTTCCTACAGAGAATCCTAATGATA  
ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCCAGGTG  
CCCGCCGTCGTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGCTGGGGCTTGCTCCCTCGAA  
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCAGGTACACCTTCTGCTGCTCCCCTTGGAGCCCTAGATG  
GTGGCACAGGTCCAGCCCGTGAGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCACTGCCCATCA  
AGGCTCCCCCTCCCATCTGCTAGCACGTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC  
TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGACGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC  
CAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCTTGGCCCTGGAAGATGAGGACGATGTGCTACTGG  
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG  
CTCTACTGAGGCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTGGAGGTGGGTGAGCCTCCCCTCC  
ACCACTTCCCTTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCTCCCGTTGACCTTATGTAGCTGCTATAAAGT  
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT  
TCACCACCACCTGCTCCCCACGCCACCACTTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA  
GGTCTGGACACTCCATCCTTGCCAAACCTTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAACCTAGAGA  
CCCTCCAGCCCCCAAGGGGAGGATTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG  
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA  
GGAATCATACATCTC



## **FIGURE 68**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTQLQRPLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP  
MGQGFLLSYSQDWLMCLQEETFQCLNHRCSVSAVQRCGDVDACGDGSDEAGCSSDPFPGLTPRP  
VPSLPCNVLTLEDYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRRLAVRFTALDLGFGDAVH  
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP  
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT  
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPD CADGSDEWDCS  
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY  
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRLMRRLVR  
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA  
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLP SLGPPGPTRSPPGPHTAV  
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

0978192.101501

## **FIGURE 69**

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACCTTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAAAAGAAGTTTTGTAATTTTATATTACTTTTTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

09978192.101501

## **FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTEFFIIAQAPEPYIVITGFEVTVILFFILL  
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

### **Important features:**

**Potential type II transmembrane domain:**

amino acids 26-42

**Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

**Leucine zipper pattern**

amino acids 78-99 and 85-106

**N-myristoylation site.**

amino acids 110-115

**Ribonucleotide reductase large subunit protein**

amino acids 116-127

## **FIGURE 71**

GGGCGAGAAGTAGGGGAGGGCGTGTTCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC  
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATAACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

## FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG  
CTGGGCGCGCCCCCGGGCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC  
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG  
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCCACCCCGGGACCCGGGACCCC  
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG  
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT  
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC  
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC  
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT  
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG  
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG  
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG  
CTGGCGTGCTGGACGAATTTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTACGC  
CCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCATCCACAAAT  
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCAGAA  
GAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG  
CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT  
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCTGAGGTCGTCA  
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA  
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG  
CTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTAC  
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA  
AAAAAAACTTCATTCTAA

## **FIGURE 73**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL  
ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS  
YIDTYFDTERSSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF  
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLLR  
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSRSFR  
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA  
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLIVLLLLLPFRC  
QRRPRDPEVVNDESSLVRHRWK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 466-494

#### **N-glycosylation sites.**

amino acids 170-173 and 366-369

#### **Leucine zipper pattern.**

amino acids 10-31 and 197-118

#### **Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

## FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG  
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCTGGGCGGGAGCCGGGAGGCGCGGCC  
GGCATGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA  
CAACCTGGTGAAGGCCCCGCGGTGCGGCGGCATGGGCAACCTGCGGGGCGGCACGGCCGTGG  
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG  
CGCGTGGTGTGCTGGCCTGCCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA  
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC  
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT  
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCTGAAGGCATGTGCCCTAGCCGCG  
TGGTGGTGGTAGCCTCAGCTGCCCACTGTGCGGGACGTCTTGACTTCAAACGCCTGGACCGC  
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT  
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC  
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTTGATGGCTGCGCCCACTTTTG  
CGCCCATTTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGGTGCCCAGACACCCCTGTATTG  
TGCTCTACAAGAGGGCATCGAGCCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG  
AGGTGCCTCCAGCTGCCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG  
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC  
AGAGGCCCCATCTTCTCTAAGCACCCCCCACCCTGAGGAGCCCACAGTTTCTCAACCTTACC  
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG  
CCTGAGATCCAGCTCTCTAAACCCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT  
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC  
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT  
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT  
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG  
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG  
TGAACCTGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG  
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG  
GGATCTGAACCCAAGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA  
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG  
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAAA  
AAAAAAAAAAAAAAAAAAAA

## **FIGURE 75**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGA YVLVYYNLVKAPPCGGMGNLRGRTAVVTGANS  
GIGKMTALELARRGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLS  
SEPRLDILIHNAG  
ISSCGRTREAFNLLLRVNHIGPFLLTHTLLLPCLKACAPSRVVVVASAAH  
CRGRLDLDFKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCTAAHPGPVNSELF  
LRHVPGWLRPLLR  
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARD  
DRAAHLWEASKRL  
AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSPQSSPD  
LSKMTHRIQAKVEP  
EIQLS

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Glycosaminoglycan attachment site.**

amino acids 46-49

#### **Short-chain alcohol dehydrogenase family**

amino acids 37-49 and 114-124



# FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG  
GACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC  
CAAGCCTCAGGCCAGCCACCTCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCGTAGCATGGTGCCCCCAGAC  
CCACACCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACGATGGCCAG  
GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCT  
CGGCTGTCTGTGGCTGTCTCCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG  
TTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG  
GCCCTCCAGCCCCGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG  
ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCC  
CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTAGCTGGAAAATGTGACACTGCTGAACCCGGAT  
CCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTGAGTGGCCCTGCTGCGCCTGCCCAA  
TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC  
GGCTGGCAGAGCGCAGAGCTTGGAGGCCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC  
CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGGAAGTGGCCAGTGCCCCACCTCAGGAA  
GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCAATGGCATC  
ATCCGTGGCTACCAGGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAACTGGACTGTAGTTGGTGAGCAG  
AGCTCCTCAAATGAGCTCGCCACCCATATGCCAGGCTCCTACTGCGTGCAAGTGGCTGCAGTCACTGGTGCTGGAGCT  
GGGGAGCCCCAGTAGACCTGTCTGCCTCCTTTTAGAGCAGGCCATGGAGCGAGCCACCCAAGAACCCAGTGAGCAT  
GGTCCCTGGACCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCCTGAGGTCACTGCCACCTGCGGTGTTGCACCTC  
TGGCTGCTGCTTCTGGGCACCGCCGTGTGTATCCACCGCGCGCGGAGCTAGGGTGACCTGGGCCCAGGTCTG  
TACAGATATAACAGTGAGGATGCCATCCTAAAACACAGGATGGATCACAGTGACTCCCAGTGGTTGGCAGACACT  
TGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCAGCAGCAGCCTCAGCAGTCCGGCTGGGGGCGGATGCCCGG  
GACCCACTAGACTGTCTGCTCCTTGCTCTCCTGGGACTCCCAGGCCCGGGCGTGGCCCTGCTTCCAGACACC  
AGCACTTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCCAGGTCCCAGCT  
GTCAGGCGCCTCCACCCCAGCTGGGCCAGCTCTCCAGCCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCGAGG  
GGACTCTCTTCTCCCCGCTTGTCTCTGGCCCCGTCAGAGGCTTGAAGGCCAAAAGAAGCAGGAGCTGCAGCAT  
GCCAACAGTTCCCCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCCTGTGAGTTAGGAAATAGAGGTTCC  
AAGAACCTTTCCCAAAGCCAGGAGCTGTGCCCCAAGCTCTGGTTGCCTGGCGGGCCCTGGGACCGAAACTCCTC  
AGCTCCTCAAATGAGCTGGTTACTCGTCACTCCTCCAGCAGCCCTCTTCTCATGAAACTCCCCCAACTCAG  
AGTCAACAGACCCAGCCTCCGGTGGCACCAAGGCTCCCTCCTCCATCCTGCTGCCAGCAGCCCCCATCCCCATC  
CTTAGCCCCCTGCAGTCCCCCTAGCCCCCAGGCCTCTTCCCTCTCTGGCCCCAGCCCAGCTTCCAGTCCGCTGTCC  
AGCTCCTCACTGTCTATCCCTGGGGGAGGATCAAGACAGCGTGCTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA  
CTCAGTGAGGGTGAGGAGACTCCAGGAACAGCGTCTCTCCCATGCCAAGGGCTCCTTACCCCCCACCACCTAT  
GGGTACATCAGCGTCCCAACAGCCTCAGAGTTACGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCAAGGGG  
GGAGTCTTGCTGTGCCCCACCTCGGCCCTGCCCTCACCCCCAGCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC  
TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGTCTCTCCGATGGCTCCTTCTCTCGCTGAT  
GCTCACTTTGCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCCGGTCTAGAGCCCAGGGAGGCAGACTGC  
GTCTTTCATAGATGCCTCATCACTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCCTGCCCCTG  
TGGGAGTGAGGGCCAGACTGGTTGGAAGACATGGAGGTCAGCCACACCCAGCGGCTGGGAAGGGGGATGCCTCCC  
TGGCCCCCTGACTCTCAGATCTCTTCCCAGAGAAGTCAGCTCCACTGTGCTATGCCCAAGGCTGGTGCTTCTCCT  
GTAGATTACTCCTGAACCGTGTCCCTGAGACTTCCCAGACGGGAATCAGAACCCTTCTCCTGTCCACCCACAAG  
ACCTGGGCTGTGGTGTGTGGGTCTTGGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG  
TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA  
ACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCCACCACAGGTGTGTTTGGC  
CTGAGGAGCAGCCCTGCCTGCTGCTCTTCCCCCACCATTGATCACAGGAAGTGAGGAGCCAGAGGTGCCTTT  
GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGGAGCCCCCTCTCAGCCTTACCT  
GGGCCCCCTCTTAGAGAAGAGCTCAACTCTCTCCAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTG  
AGGCAC'TGAGGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGGAG  
TATGAGACCGTAGGTCAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATACCATAAAAT  
GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09978192-101501

## **FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP  
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM  
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCV  
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV  
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG  
PDSNVLLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD  
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST  
FYGSLIAELPSSTPARPSPQVPAVRRLLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA  
WKAKKKQELQHANS SPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAVRALGPKLLS  
SSNELVTRHLPPAPLFPHETPPTQSQQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS  
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGSLANGWGSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPDYS

### **Important features:**

#### **Transmembrane domain:**

amino acids 448-467

#### **N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

#### **N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

#### **Phosphotyrosine interaction domain proteins**

amino acids 740-753

## FIGURE 78

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT  
CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT  
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA  
ACCTCACCTTGCAAGACGCTGGGGAGTACTGGTGTGGGGTTCGAAAAACGGGGCCCCGATGAG  
TCTTTACTGATCTCTCTGTTCTGTTTCCAGGACCCTGCTGTCCTCCCTCCCCTTCTCCCAC  
CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC  
CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
GCTGAGGCCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGC  
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTTGGTGCTGCTGAGCCTTCTGTTCAGC  
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTGCGGAGGAAAAGGAAGCC  
CCTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCCTCCACACATCTGAGGAGGA  
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT  
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
TCCAGCTGCCCCGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGATGTTCCA  
GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA  
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC  
CTCATGCCAGTGTGCGACCCCTGCCTTCTCCTCCACTCCAGACCCACCTTGTCTTCCCTCCC  
TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTATGAAGAGGAGCATGCT  
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT  
GTGAAAAACGTGATTCTTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
GACTCTGAATTCTAACAATGCCAGTGACTGTGCGCACTTGAGTTTGAGGGCCAGTGGGCCTG  
ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC  
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG  
TCCAGGCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG  
TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA  
AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA  
GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTCGGGGGTGGTGGTAAAGTA  
GCACAACACTACTATTTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT  
GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCCTCCTGGGTTCAAGTGATT  
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT  
TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCCTGAC  
CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG  
TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCAGTATGCAAACTTGGAAAG  
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT  
TATTTTCGTTTTGTTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT  
TTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
ATCACTTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTTTATAAATAAAATGTTTCATCA  
GCTGCATAAAAAAAAAAAAAA

## **FIGURE 79**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGP EEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSI RDSRQELSLIVTLWNLTLQDAGEYWCGVEKRGPD E SLLISLFV  
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
LAPVLVLLSLLSAAGLIAFC SHLLLWRKEAQQATETQRNEKFWLSRLTAE E KEAPSQAPEGD  
VISM PPLHTSEEEELGFSKFVSA

### **Important features:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 248-269

#### **N-glycosylation site.**

amino acids 96-99

#### **Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

#### **Ig like V-type domain:**

amino acids 13-128

09978192-104504  
TOSTOT-2678660

## **FIGURE 80**

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG  
CTACATGACTTCGGGCTGGACGGATAACGGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTTTACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC  
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC  
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGGAAATGTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA  
AAGGATGGTTGAACGTGAAA

## **FIGURE 81**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCSNLTTPNVPNVCRMYSDDLNPNLKDTVICAMKITQEPQGLGY  
WEAWRHHCQGKDLTEWVDGPDF

**Important features:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 67-72

**Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

09978192-101501

## FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCTGCGTTC  
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA  
AGCTGTCTGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC  
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAGTGTCTCCACAC  
TCGACTCCTTGCCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTTCGTG  
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCT  
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCACAGGGCTTCCAGTGGTCAG  
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG  
GAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTCAGGCTCCTGTG  
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG  
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGAGCCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGTGGGCACGAGGGGCCGCACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGCTGCTTCGTCAAGTGCCGGC  
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCCGCCTGCCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA  
GATACTGGTTGTATTTTTTGTCTGGTTTGGTTTGGGTCTCATGTTATTTATTGCCGAA  
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT  
GCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTCTCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA  
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACTCTCCAGCACACA  
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATACCAGGTCAAGGGCACCAAGGTTCAATTCAGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA  
GTCCCACCCTAGAACCAGCCTGCCCCAGCCTGCCCCCTGGGAAGAGGAACTTAACCACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT  
TGCAGTCATGCCCCGAGTCACCTTTCACAGCGCTGTTCTCCATGAAACTGAAAAACACACAC  
ACCTGCGAGA  
GAGAGGGAGGAAAGGGCTGTGCCCTTTCAGTCATGCCCCGAGTCACCTTTCACAGCACTGTTCTC

0978192-101501

## **FIGURE 83**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSRLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE  
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSL PVFGKVVTQGTREAAFVYAISSAGVAFV  
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM  
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR  
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC  
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 88-91 and 297-300

#### **Wnt-1 family signature.**

amino acids 206-215

#### **Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

09978192.101501



## FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC  
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC  
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG  
GTGCCCTGAAGGAGGAGGTCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG  
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGGAAGTGCCTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG  
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC  
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG  
GCTGTGCGCCATCTGGGCAAGGTTCAAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAAGTGTGTCATGATGC  
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAACCTGCTTGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCGTA  
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCCT  
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC  
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC  
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA  
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

09978192-101501

## **FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGSSEEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA  
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAEELGEAQAKLMEQESALR  
ELRERVTOQLAEAGRGREDVRTELFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW  
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS  
HWNQGEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 31-54

#### **N-glycosylation sites.**

amino acids 73-76 and 159-162

#### **Leucine zipper pattern.**

amino acids 102-123

#### **N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

#### **C-type lectin domain signature.**

amino acids 264-287

## FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG  
GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCCTTTCTCCCACGTCCTATCTGCCTCTCG  
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTGGCCGGCCCGG  
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCAGCCCCGGCCGCGCCCTGGGCAAG  
GCCCTCTGCCTCTCCTCCTGGCCACTCTCGGCGCCGCGGCCAGCCTCTTGGGGGAGAGTC  
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA  
CGGCCTTCCCCAAGCAGTACCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCACTAACGGGCTGCG  
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACG  
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC  
CAGCCCCGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG  
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC  
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCCAG  
CCACCCGGCCAACCTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA  
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC  
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAACGCCGCTGGACTGCGAGGTCTC  
CCTGTGGTTCGTCTTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA  
CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCCTGCCCGAGCTCGAAGAAGAG  
GCTGAGTGCGTCCCTGATAACTGCGTCTTAAGACCAGAGCCCCGCAGCCCCTGGGGCCCCCG  
GAGCCATGGGGTGTGCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG  
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT  
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG  
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC  
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCTTTCATCG  
TCCAGGGGCGCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG  
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG  
TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT  
GTTGCTCACAAAAA

## FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL  
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAEERGEAWALMKEIEAAGEALQSVHEVF  
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVSPDWFVGVDSLDCDGRWREQAALDLYP  
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP  
RAFIPPAVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA  
NNGSPCPELEEEAECVPDNCV

**Important features:**

**Signal peptide:**

amino acids 1-26

09978192-101501  
TOSTOT-26181660

## FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA  
TATTGACAAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA  
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC  
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAAATA  
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT  
ATCCAACCTTTGTTTGAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTTTATTACCGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA  
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTGAGCAGATGAACT  
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC  
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT  
GAGGTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAGA  
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT  
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG  
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT  
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAAA  
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAACGGGAACCTTTAGCAG  
CAAAACAAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA  
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG  
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT  
TTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA  
ATAAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATATAAAT  
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG  
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG  
AAAAACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG  
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT  
TCCACAAAAA

## **FIGURE 89**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK  
PEEEVKKLKPKGTKNFSLLSFGEAAEEEEEEVN RVVSQSMKGKSKSSHDLKDDPHLSSVPVV  
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK  
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK  
DASMQSDTFEIYDPRNPVKNRRREESKKLMREKKERR

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 109-112 and 201-204

#### **Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

#### **Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

09978192.101501  
TOSTOT.2678660

## FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG  
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTGCGCTTGCTGACGGCGTCG  
AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC  
GTGGCCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA  
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG  
CTCCTTCAAGTGTTTGGAAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACCTCTA  
GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC  
CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTATAGGAGTCCCTT  
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAA  
GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTCGCCAGGCTGGAG  
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCCTGC  
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG  
ATGTACGTACGACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT  
GAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCAGCTGCCAGTGATGGTCTGGTTCC  
CGGGAGGCGCCTTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC  
GAGAAAGTGGTGCTGGTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTGAGCACGGA  
CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC  
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTTCGGCCAGTCGGCG  
GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC  
CATTTCCCAGAGTGGCACCGCGTTATTTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG  
CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC  
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAC  
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGT  
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA  
ACCGTATGATGGACATAGTTCAAGATGCCACTTTTCGTGTATGCCACACTGCAGACTGCTCAC  
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA  
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC  
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC  
TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA  
TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT  
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC  
TGACATCCCATGATGCCCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC  
ACCACACTGTGCTCAGCTCTCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT  
CCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGTTCGACCCAGACTGCCACTGC  
CCCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGCTCAACCTTGTTCTGTCTGT  
TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTTGGGA  
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAGTCTATACACAGGGGTGG  
TCTCTTCAATAAAGAAGTGTTGATTAGAAAAA

## **FIGURE 91**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG  
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGT LQ GKQMHVGKTPIQVFLGVPF SRPP  
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS  
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA  
AFGGDPGNVT LFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLAGCNHNSTQILVNCLRALSGTKVMRVS NKM RFLQLNFQRDPEEIIWSMSPVVDGVVIPDD  
PLVLLTQ GKVSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMMD  
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

**Important features:**

**Signal peptide:**

amino acids 1-29

**Carboxylesterases type-B serine active site.**

amino acids 312-327

**Carboxylesterases type-B signature 2.**

amino acids 218-228

**N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468



## FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT  
GCTGTCTCTGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG  
AGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA  
CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC  
CAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC  
GATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAGTGTCTCTTGGTGATCAGAGACGCGCAG  
ATGCAGGATGAGTCACAGTACTTCTTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTT  
CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCCAGGACC  
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC  
GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTATCAGCATTTTACGTGACAACAC  
GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCCAAAAGGCCAGT  
TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTCTGCAG  
AACAGAGTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG  
GGTGAAGGCTGGGGATTGAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC  
AGCGAGCCCTGGACCTCTCTGTGCACTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA  
GCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA  
AAGCCTGTGCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA  
GGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGTCTCTGGAGCTGCCTCGGGTT  
CAAGTGGAGCACGAAGGAGAGTTTACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGT  
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTTCTCAACGGAG  
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGCGCCTGATCATCATGAAG  
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAC  
GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA  
AAGCCACACCAAACAGTCCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAG  
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCCAGAACCCAAATCATCCACTCAAGC  
CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA  
GACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAAGTCAAGTTC  
CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTTCGGCTAGGGAGGAAGGTAGAGTAAGAG  
GTTGAAGATAACAGAGTGCAAAGTTTCTTTCTCTCCCTCTCTCTCTCTCTTTCTCTCTCTCT  
CTCTCTTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC  
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGCGGAGTTGAGACCCAGCCTG  
GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG  
CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG  
AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA  
TCTCAAAAAAAAATCCTCCAAATGGGTTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTA  
AGGTGGGTGGATTGCTTGAGCCCAGGAGTTGAGACCCAGCCTGGGCAACATGGTGAAACCCC  
ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGT  
CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC  
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG  
TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAA  
ATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTGCTCCTCACTGCTACACTCCT  
GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA  
AAAGGGGGAGGAATGAATAATCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA  
GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT  
TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAA

## **FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFYPRQDWTGSTPAYGYWFK  
AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAGNCSLVIRDAQMQDESQYFFRVERGS  
YVTYNFMNDGFFLKVTVLSTFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL  
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLVQYPPENLRVMVSQANRTVLENLGNGTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQSPDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP  
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

**Important features:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins  
signature.**

amino acids 365-371

09978192-101504  
TOSTOT-26T8660

## FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAACTGTTATTTACTGCTGCGTTT  
TATGTTGGGAATTCCTCTCCTATGGCCTTGCTTGGAGCAACAGAAAACTCTCAAACAAAGA  
AAGTCAAGCAGCCAGTGCATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT  
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA  
CAATGGAAACAATTCCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC  
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA  
GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT  
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAATGGATAGAGAAC  
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
TCTGGAACAACAAGTGATTATAATTAACTTTTCAGATGTTAATGACAATAAGCCTATATTTAA  
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT  
GATTCGCAAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAA  
AAAGAAAGTGGATTTTGTAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC  
ATGTTCTTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACCTTTCATTAAGATCCAG  
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGA  
AGAAACCCACAGGGATCATTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT  
CTCCTATCAGGTATTCTATTACTAGGAGCAAGTGTTCAATATCAATGATAATGGTACAATC  
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC  
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA  
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT  
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT  
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTTACAATCATAGATAATCAAG  
ATAACACAGCTGTCAATTTTGTACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCCTGTCTTC  
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC  
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG  
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTTGCTATTCTCATTGTCATTATGATCATA  
TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAAACAACGGAGAAAAACAGATTCTATTTCTGA  
GAAAAGTGAAGATTTTCAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT  
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA  
CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG  
CCCTCTCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC  
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT  
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG  
GCTTTTTTACCATCAAAATTTTTTAAAAGTGCTAATGTGTATTCTGAACCCAATGGTAGTCTTAA  
AGAGTTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC  
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTTCATTGAACAGAGATGTG  
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAAATAATG  
TAGGAAGATATTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT  
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAAATTTAAAGGAGCAAAAATTTG  
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA  
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCTTTAT  
TTAAA

## **FIGURE 95**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKGWVWNQFFVPEEMNTTSHH  
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT  
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL  
LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLS D  
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIIITNHE  
TQEGIVILKKKVDFEHQNHYGIRAKVKNNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL  
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA  
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR  
DESIEEHHFYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP  
SLTSTNTLTIHVCDGSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ  
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY  
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLES AVSDQD  
ESYDYLNELGPRFKRLACMFGSAVQSNN

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 597-617

#### **N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

#### **Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

## FIGURE 96

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA  
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTTCGCAAACATTTGACATTATT

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## FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC  
CCAGAGCTTCTCCAGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACTTCCTCCGCGGGG  
CCCAGCCACCTTCGGGAGTCCGGGTGCCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCA  
CCCCTGAGCCAGCGCGGGGCCCGAGCGAGTCATGGCCAACGCGGGGCTGCAGCTGTTGGGC  
TTCATTCTCGCCTTCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG  
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA  
TGTCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT  
CTGAGCAGCACATTGCAAGCAACCCGTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT  
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC  
AGAAGATGAGGATGGCTGTCTATTGGGGGTGCGATATTTCTTCTTGAGGTCTGGCTATTTTA  
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCAGT  
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC  
TTCTGGGAGGTGCCCTACTTTGCTGTTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA  
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACACAGAGGCAAAAAG  
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAACATTAGGAC  
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAA  
ACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTCTCA  
ATATAGGAGGGAAGATTTTTCCATTTGTATTACTGCTTCCCATTTAGTAATCATACTCAAAT  
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAA  
ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAATATCTCTAAAT  
AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC  
TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCTTTG  
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTCAATTCTTCATGCGTGCCCTTTT  
CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT  
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTCATAGCCTACATTTTA  
GTTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAATCTTTCTGCATG  
ACCAAAGTGATAAATTCCTGTTGACCTTCCACACAATCCCTGTACTCTGACCCATAGCACT  
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT  
AACACAACCTTTATTGATTGAATTTTTAAGCTACTTATTTCATAGTTTTATATCCCCCTAACT  
ACCTTTTTGTTCCTTAAATTGATTGTTTTCCCAAGTGTAATTATCATGCGTTTTTA  
TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT  
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA  
TTAGTTTATATTACTCTTATTCTTTGAACATGAACTATGCCTATGTAGTGTCTTTATTTGCT  
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT  
CACTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT  
GTGGTTCAGTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC  
CTTCATGTGGCTCAGTGCCTTCCTCTCTCTACCAGTCTATTTCCATTCTTTTCTGCTGTGTCT  
GACATGTTTGTGCTCTGTTCCATTTTAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG  
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG  
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA  
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCCACCTCACAGTGATG  
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAAGTGCTAT  
ACTAAGGGAAAGAATTGAGGAATTAACCTGCATACGTTTTTGGTGTGCTTTTCAAATGTTTGA  
AAATAAAAAAATGTTAAG

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI LAFLGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQI  
QCKVFDSSLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDDEVQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQEFYDPMTPVNARYEFGQALFTGWAAASLCLLGALLCCSC  
PRKTTSYPTPRPYPKPAPSSGKDYV

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

#### **N-glycosylation site.**

amino acids 72-75

#### **PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

#### **ABC-2 type transport system integral membrane protein**

amino acids 119-133

## FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC  
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC  
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN  
CNTTCAACANTTCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA  
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCTGTCCC

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## FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA  
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGACGGTCTGGCTA  
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

## **FIGURE 101**

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTTGAACGTGNGCGTGTGCGAGANCACCGGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT  
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCCTGCGA

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## FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT  
GCNTGTTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAGTCAATG  
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG  
GGAGGTGCCCTACTTTGCTGTTTCCTGTCCC

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## **FIGURE 103**

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGACAGGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCCAGTCAATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC  
CCTACTTTGCTGTTCCCTGTCCCCGAA

## **FIGURE 104**

AGCAATGCCCTGCCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA  
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT  
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA  
ATTTTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG  
GCTGGGCTGCTGCTTNTTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTGCGAACC

## **FIGURE 105**

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCCAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTTGCTGTTCTG

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## FIGURE 106

TTCTTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC  
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGACAGGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

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## **FIGURE 107**

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA  
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA  
TGACGAGGGGCTGTGGATGTCNGCGTGTTCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTTCATTGGGGGCGCGATATTTCTTCTTGC  
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT  
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC  
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTGCGAA

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## FIGURE 108

GCCTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC  
CGCGTAGACCGACCCCCCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCCCCGTGCCCG  
ACCGGTCCCCGCCTTTTTTGTAAAACTTAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCCGGT  
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG  
CAGGTCCTGAGCCTCGAGCCGCGAGCACGAGCTCAAATTCCGAGGTCCCTTCACCGATGTTGT  
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA  
CAGCACCACGTAGGTACTGTGTGAGGCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT  
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT  
TATGGTTCAGTCTATGTTTGCTCCAACCTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
CAAAACCGGAAGACCTTATGGATTCAAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT  
GATAAACCACATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAAGACAGAAAC  
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAGCAGTTCAAG  
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTTCAGCATTAGC  
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTTGTCTTTA  
TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTTAGAGGTAGCATGCACAGGATGGTAAATTG  
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT  
AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC  
AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG  
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT  
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGTGGATTACCTC  
TCTTAAATGACACCCCTTCTCGCCTGTTGGTGCTGGCCCTTGGGAGCTGGAGCCCAGCAT  
GCTGGGGAGTGCAGGTGAGTCCACACAGTAGTCCCAAGTGGCCACTCCCGGCCAGGCTG  
CTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA  
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGTATTATTCAGAGATGTTTAAATGCATA  
TTTAACTTATTTAATGTATTTTATCTCATGTCTTCTTATTGTGACAAGAGTACAGTTAATGC  
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT  
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA  
GGAAGTGTTTTTTCTGGGTGAGTAAATAACAACGTGCATAGGGAGGGAAATTCTCAGTAGTG  
ACAGTCAACTCTAGGTTACCTTTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
CCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC  
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC  
TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCAGTTCTGTTTGA  
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCCCCAAAATTAAGAAAA

## **FIGURE 109**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID  
AGASINVSVMQLQPFDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRCVFE  
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKEEDGLRMRKTVQSNSPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

**Important features:**

**Transmembrane domain:**

amino acids 224-239

**N-glycosylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

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## FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAGAATTCTTTTGTCATTTTGTACATTTGCTCTATGGGGGAATTATTATTTT  
ATCATTTTTATTATTTTGCCATTGGAAGGTAACTTTAAAATGAGC

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## **FIGURE 111**

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCCAGGCTGCTTT  
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA  
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

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## **FIGURE 112**

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT  
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

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## **FIGURE 113**

GGTGGCCCATTTCCCGGCCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT  
GCTTTGTTCAANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTCA  
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA  
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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## **FIGURE 114**

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGTATTATTCAGAGATGTTTAATGC  
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA  
TGCTGCGTGC

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TOSTOT-26T82660

## **FIGURE 115**

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACNTGNGT  
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC  
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA  
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTTCANTT  
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTCAGAGATG  
TTTAATGCATATTTAANTTATTTAATGTATTTTCATNTCATGTTTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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## FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC  
CACGTGGCCCACTCCCGGGCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC  
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA  
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTTC  
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT  
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

## FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCGGCCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA  
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC  
CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCCAGGCTGGAGTTCAGTGCCA  
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA  
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTTTCACC  
CCTGGGTGGACCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
GGTACCCCGGATTGTGAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG  
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC  
CTTTCTGAATTGGAGGATTATCTTTCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT  
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG  
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGTTTCAGCATCTTGACAAA  
AGGTTCTTAACCAATTTCCCTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
TCTCATTTCCCCTCAGCATGTTCTAACTGCTGCCCACTGTGTTTCATGATGGAAAGGACTATG  
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAGAGAGAGGGTAC  
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTC  
AGAGGATTGCCGAAGGGAGGCCCTTCCCTTTCAGTGGACCCGGGTCAAGAATACCCACATTCCG  
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGAATGACTATGCTCTTCTGGA  
GCTGAAGCGTGCTCACAAAAAGAAATACATGGAACCTGGAATCAGCCCAACGATCAAGAAAA  
TGCCTGGTGGAAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT  
CGGTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC  
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC  
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTTCAGAAGGAC  
TACAACGTTGCTGTTTCGCATCACTCCCCTAAAATACGCCCAGATTTGCCTCTGGATTCACGG  
GAACGATGCCAATTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA  
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT  
GAACTCTGTCAATAGCATTTC AACATTTTTC AAAATCAGGAGATTTTCGTCCATTTAAAAAA  
TGTATAGGTGCAGATATTGAAACTAGGTGGGCACCTTCAATGCCAAGTATATACTCTTCTTTA  
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTTCCTTCTTAAAAATTAGACACACTTT  
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC  
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA  
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA  
CTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT  
GGGACATTTAGTTTAGTTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA  
CAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTAAAAAA  
TGGGAGAAATAGTTTGTTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT  
TAAGATCTCAAGTTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG  
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT  
TCTATGTATGAGGTGCTACATTTT TAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT  
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG  
TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

## **FIGURE 118**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTP<sup>g</sup>WT<sup>l</sup>LIDGSEMEWDFM<sup>W</sup>HLRKVPRIVSERTFHLTSPA<sup>F</sup>EADAKMMVNTVC  
GIECQKELPTPSLSELEDYLSYETV<sup>F</sup>ENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV  
YGTDSRFSILD<sup>K</sup>RFLTNFPFSTAVKLSTGCSGILISPQHVLTA<sup>A</sup>HC<sup>V</sup>HDGKD<sup>Y</sup>VKGSKKLRV  
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKSGRGQRIAEGRPS  
FQWTRVKNTHIPKGWARGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS  
GFDNDRADQLVYRFCSVSD<sup>E</sup>SN<sup>D</sup>LLYQYCD<sup>A</sup>ESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

**Glycosaminoglycan attachment site.**

amino acids 236-239

**Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

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## FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCATGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC  
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG  
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAAGGAACAACCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT  
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCTTGATCACTT  
ATATCTGGAAACCAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTTCGTAACCTCGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC  
TCGTGTGGGGGGGGCATCCAGAGCCGGGAGGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACCTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCCAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA  
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTGAGAGGAGCCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATA  
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA  
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA  
AAAAAAAA

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## **FIGURE 120**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYS LRRCLS  
SKSCEGRNIRYRTC SNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSLKCQ  
AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLV LKGPDLHLYLETKTLQGTKGENSL SSTGTFL  
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP  
ATCGGGYQLTSAECYDLRSNRV VADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD  
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK  
EKLPVEAKLPWFKQAQEELEEGA AVSEEPS

**Important features:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

## FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGGTGGGCCCTCGGGCCTGAC  
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG  
GCCCCCGGTTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT  
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG  
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG  
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA  
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGGACTCCTCAAAAGTTCAGCTCCCAGCA  
GGATTGTGGTAGTTTCTTCCAAACTTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTTGTATATAGCCGGAGCAAACCTGGCTAACATTCTTTT  
TACCAGGGAAGTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTGATGGGCTTTTTTCAAACTCCAGTAGAAGGTGCCCAGACTTCCATTTATTT  
GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAGGAAGATACTTTGGGGATTGTAAAGAGGAAG  
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAACTCTGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAAAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAGAATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAATTATTTT  
TGGGATAAGAGAATTTTCAAGCAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA  
GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA  
ATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTTACTACAATGTTTGGTGTTTGTGTGGAAATTATCTGC  
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTAC

## **FIGURE 122**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEAAAGQLRREL RQAAECGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNH LGHFLLTNLLLGLLKSSAPSR  
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSR SKLANILFTRELARRLEG TNVTNVNLHPG  
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDESVARKLWDISEVMVGLLK

**Important features:**

**Signal peptide:**

amino acids 1-21

**Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

**N-glycosylation site.**

amino acids 212-215 and 239-242

## FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT  
TGAAGAAAAAGAATTTTGTATTTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TTACTGAAAAATTATTTTGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATACTGGGCA  
AGCATGGATGACATATTAATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT  
TGTGTGGAAATTATCTGCCTGGCTT

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## **FIGURE 124**

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCCAGCC  
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC  
CCCAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT  
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA  
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT  
TCCAAATGAAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC  
AGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAG  
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAG  
TGACCCCATTC AAGAAATTCGGGACTTAGCAGAAATCACC ACTCTTGATCGCAGCAAAAGAA  
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACA ACTATAGAGTTTTTGAACGAGTAGCG  
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAAACCGGAAAG  
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT  
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT  
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCAGAAATGAAGTAGCTCGGC  
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT  
CCTCTTCTGCACATACAGAAA ACTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG  
GCATATGTATGTGTTTGGGAGACTTCAAAGATGTATTAATTCCTGGAAA ACTCAAGCAATTCTG  
TATTTGACTTACATTCTGGAAA ACTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT  
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA  
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAAACTTG  
AAAAACAGTTTGTAAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA  
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
AAAAA

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## **FIGURE 125**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPTTTEITSLATENIDEILNNADVALVNFYADWCRFSQ  
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYR  
GQRSVKALADYIRQQKSDPIQEIRD LAEITTLDRSKRNIIGYFEQKDS DN YRVFERVANILH  
DDCAFLSAFGDVSKPERYS GDNIIYKPPGHSAPDMVYLGAMTNFDVTYNW IQDKCVPLVREI  
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH  
IQKTPADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG  
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

**Important features:**

**Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

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105101-26181660

## **FIGURE 126**

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

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## **FIGURE 127**

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTGCGCCGCNNGGAGCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCCTTTCCTAACCC  
AACCCAACTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC  
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTACTCCTGTAACAACCTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTGTTTTAGTCAG  
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA  
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA  
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTTGGCAGATTACATCAGGC

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## **FIGURE 128**

GCCCACGCGTCCGATGGCGTTACGTTGCGGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCCTTGTA TCTCCCAGAGTACCTCAT  
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA  
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG  
GTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTG  
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT  
GATTACCTCTGGTGTTGACAGGTTTGAACCTTGCACTTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTA  
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA  
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTTATTTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG  
TACTACAGATTTTCAAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTTAGT  
GCAATACAATAAAACTCTGAAATTAAGACTC

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## **FIGURE 129**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF  
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFYYLYGMIYVLVSS

**Important features:**

**Signal peptide:**

amino acids 1-20

**Type II transmembrane domain:**

amino acids 11-31

**Other transmembrane domain:**

amino acids 57-77 and 123-143

## **FIGURE 130**

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG  
AATCCCCTTGTA CTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTTGGCATATCATATTTGGAGGTATA  
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT  
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT  
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACACACACAGAAGAATT  
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

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## **FIGURE 131**

CGGACGCGTG GGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC  
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCTGGGGACCGCTTCGGCTGAAGCATTGAC  
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACAC  
CTACCCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC  
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA  
GAAGCATATTCCTAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC  
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC  
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA  
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA  
GAAAGTGATGGCTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT  
TGTCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAATGAAGATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT  
AAAAGACAAGTGTAATAGACATCTAAAATTCCTCTCATAGAGCTTTTAAAATGGTTTCA  
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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## **FIGURE 132**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRAQLTYPLHTYP  
KEEELYACQRCRLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCQNQLPFA  
ELRQEQLMSLMPKMHLLFPLTLVRSFWSMMDSAQSFITSSWTFYQLQADDGKIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSYLOMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG  
PLPTKVNLAHSEI

**Important features:**

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site.**

amino acids 90-93

09030102-101504

## **FIGURE 133**

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTTCGC  
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

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## **FIGURE 134**

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTTCGGGGACCG  
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG  
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT  
CCGC

09978192-101501

## FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT  
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC  
GTGCGGACTGGCCTCCCAAGCGTGCGGGCGACAAGCTGCCGGAGCTGCAATGGGGCCGCGGCTG  
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC  
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTTGATGATTGT  
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA  
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTTTCT  
GGAATGACATCAGCCAGTGTGGAAGAAGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
GTTCTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA  
AGAATGTGAACAAGCTGAACGACTTGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC  
ATTCAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
CAAGGGACCAGATGCTTGGAATAATGGAATGTCATCTACGAAGAAAAGTGTTTTAAGCCAC  
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT  
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTTCTACAGACTTATATCTGG  
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG  
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGAAGTAA  
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT  
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC  
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCTTTG  
CATTTTGATGAGAATTCATTTTTTTGCTGGGGATAAAAAAGAAGCACACAACTAAAGGAGGA  
CTTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC  
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG  
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCATCTAACCAGACAAGA  
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAC  
TCAGGAACCTGTTACAGAATATTCATTAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC  
AATGGAGGCGAAAGAGTGGAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA  
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT  
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG  
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAQRCFCQVSGYLDDCTCDVETIDRFNNYRLF  
PRLQKLLESDYFRYYKVNLRPCPFWNDISQCGRRDCAVKPCQSDEVPDGIKSASYKYSEEA  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP  
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAF  
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI  
ELRALSKVLPFFERPDLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 280-283 and 384-387

#### **Amidation site.**

amino acids 94-97

#### **Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

#### **Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

#### **Interleukin-7 proteins**

amino acids 338-343

09978192.101504

## **FIGURE 137**

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT  
CTTNGAGCGCCCAGATTTTCAACTNNTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA  
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA  
TTTTTTTGCTG

## **FIGURE 138**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC  
CGATCAGGCATGGAACCTCCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCTTGACAGG  
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGGCCACCAGAAG  
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC  
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG  
GGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC  
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC  
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAAGAGAA  
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAGCAAA  
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCCCTCTCTGGTCT  
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT  
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG  
CCTGCATGGCTATCCTCATTTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA  
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG  
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT  
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAA  
AATAATAATAATAATAATTACAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA  
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG  
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

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## **FIGURE 139**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW

DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGGFMVS

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 70-73

**N-glycosylation site.**

amino acids 98-101

**Integrins alpha chain proteins**

amino acids 67-81

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T05T07-26T82660



## FIGURE 140

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACTTTATTTTTAGCTTGCCATTGGGA  
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCTTCGTCACTCACCTGTTCTTG  
CCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT  
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGGCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTAGAGA  
CAGATGGTGATGG

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TOSTOT 25182660

## FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
ATTGAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
AATGCAGACTTTTACAAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCTCTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTTGGCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG  
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGGCCATTCCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT  
GGTCGTGCCACTGTTCTGTCTGAAAATGGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG  
TGGTCCTCCAGACACCTTGAAAATAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT  
CTCATAGGTTTTCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC  
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG  
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGAGAGAGCCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTCACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC  
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAAAAAA

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## **FIGURE 142**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLSFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHELLMWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSW  
SILKHPFNRNSTILTRPGMEITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILV  
VVPLFVWKMGRLLQYSCCPVVVLPTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation site.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins.**

amino acids 92-119

#### **Integrins alpha chain proteins**

amino acids 232-262

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## FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAAC TGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

## **FIGURE 144**

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTGGCATTGTTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT  
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCGAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGGCGAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA  
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTTACAGCGCTGCCTCCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTCT  
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCCACAGGGGCACTGAGGGGC  
AACAGGGACCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCCATGGTCGCTGAGACTCCCCTTCGAGGATTGCACCCGCCCCGTCTAAGCCTC  
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

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## **FIGURE 145**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL  
LYSHRLSELRLLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFLSRLLRDITITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE  
TVTWILIDRALNITSLQMHSRLRLSQNPSPQIFQSLSGNSRPLQPLAHRALRGNRDPRHPR  
RCRGPNYRLHVDGVPHGR

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 177-199

#### **N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

#### **Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92

## FIGURE 146

GGCGCCTGGTTCCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCGCCAGCCTCCGCCGCCGAGCCTC  
GTTTCGTGTCCCCGCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA  
GCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGC  
CGCAGAGGCGGAGGCTCGCGTATTCTGCACTCAGCACCCACGTGCCCCCGGACGCTCGGTGCTCAGGCCCTTC  
GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGCCGCTCCGGTTTGGCT  
CACCTCTCCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA  
ATCCTGAGGTCATTATTGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAACCACAGTGCTGTTTATGGCTAGA  
GCAATTCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT  
GAGTGGTGGATAGCCAAACAACGAGGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT  
AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA  
TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT  
TTGGGAGCACACTGGGGGAAGATATAGGCCCCCGACGTTTTCATGTACAATCGTGGTATGATGAAGTGAAGAGACTTT  
AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTAGGTGTTCTGGCCCTGTATGTACACATTATACA  
CAGGTGCTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTATAACATGAACATCTGGGGGCAG  
ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA  
CATGGGCGGCCCTGTTCTGCTTGGCCACCTAGTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG  
TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCAACAAGTCCATGACACC  
CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATGTTTCT  
TGTGAAGTAAGATTAAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCTGCTGGCTGTTTGGAT  
AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT  
ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTATCAAGTCCAAATAGA  
AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTACAGTCTCTAAAGTAACAGTTCAGGCTGTG  
ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTCATAAGCCTGCTTACATTGCCCCAAGAGTATACTGTCTT  
CGTAACTGTATGCAAGCAAATCCACATTAATGCTCGTGTAAATTGGAACCTCGAGTTTATTCTGATCTGTCCAGTATC  
TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA  
AAGACCTACATTGCTTCTTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATT  
AGAGTGTGTTGCTGTTGTGTAAGTGAATACTTGGAAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA  
ATTTTGTATAAACTGTAACTTACTGTACAGAGTACATCAACTATTTTTCAGCCCAAAAAGGTGCCAAATGCATA  
TAAATCTTGATAAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG  
TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT  
GTTCTACGTTTTCATATATTATATGGTGTCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG  
GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAACTGAAAGAAACCTTATCACATTTTCCCC  
AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC  
TGTTAATTTAGGCATATAGAATATTAAATCTGATATTGCACCTCTTATTTTATATAAAATAATCCTTTAATATC  
CAAATGAATCTGTTAAAAATGTTTGTATTCCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT  
ATGAAAACATTTCCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA  
AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT  
GAACAAAGATGAACTAATGTATTACATTACCATTTGCCACTGATTTTTTTTTTAAATGGTAAATGACCTTGTATATAA  
ATATTGCCATATCATGGTACCTATAATGGTGTATATTTGTTTCTATGAAAATGTATTGTGCTTTGATACTAAA  
AATCTGTAAAATGTTAGTTTTGGTAATTTTTTTTCTGCTGGTGGATTTACATATTAAATTTTTTCTGCTGGTGG  
TAAACATTAAAATTAATCATGTTTCAAAAAAAAAAAAA

09978192-101504

## **FIGURE 147**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDM  
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW  
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVWATSNRIGCAINLC  
HNMNIWGQIWPKAVYLVCNYSKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYKEGSDRY  
YPPREEETNEIERQQSQVHDTHVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTTCNR  
YECPAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHIFYIKSNRNGI  
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG  
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRV  
FAVV

**Important features:**

**Signal peptide:**

amino acids 1-20

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

**N-glycosylation site**

amino acids 28-31

09978192-101501



## **FIGURE 148**

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGGCCCGCGCTCCGACGGGGCCAGCGCCCTCCCCATGTCCCTGCTCCACGCCG  
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT  
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC  
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT  
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC  
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA  
GAATAGGGTGAAAAACCTCAGAAGGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAAGGA  
CTTTGCAGATTAAAGCCTTTC  
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG  
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCAGATGGGAGACCCATCTCTCTTGTGCT  
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTTAA  
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGA  
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGC  
TTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG  
GTCACAGCCTCAGTGCTGACTCCACAGTGGCCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT  
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT  
GGTTAATTTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA  
TTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACT  
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT  
TTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT  
GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCC  
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT  
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA  
AAAAAAAAAA

09078192-101501

## **FIGURE 149**

MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

**Signal sequence:**

amino acids 1-34

09978492-101501

## FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTTACCCCGGTCTGCGTCATGTTAAACFCCAATGTCCTCCTGTG  
GTTAACTGCTCTTGCCATCAAGTTCACCCCTCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG  
CAAAATCCGGGGCCTAAGAACACCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCCTA  
TGCTCACCCCCCATGGAGAGAGGCGGTTTACGCCCCCAGAACCCCCGTCCTCCTGGACTGGCATCCGAAATAC  
TACTCAGTTTGCTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTGGTT  
TACCGCCAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTTAAACATCTACGT  
GCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA  
TATTCATGATCAGAACAGTAAGAAGCCCGTCATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAA  
CATGATTGACGGCAGCATTTTGGCAAGCTACGGAAACGTCATCGTGATCACCATTAACTACCGTCTGGGAATACT  
AGGGTTTTTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG  
GATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC  
CTGTGTGTCAGCCTGTTGACCCTGTCCCACTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTAGAGCGGCACCGC  
CCTGTCCAGCTGGGCAGTGAACCTACCAGCCGGCCAAGTACACTCGGATATTGGCAGACAAGGTGCGCTGCAACAT  
GCTGGACACCACGACATGGTAGAATGCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC  
GGCCACCTACCACATAGCCTTCGGGGCCGGTGATCGACGGCGACGTCATCCAGACGACCCCCAGATCCTGATGGA  
GCAAGGCGAGTTCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCCCTGAAGTTCTGAGACGGCAT  
CGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG  
CTACCTGAAGGGAAAGACACTTTGCGGGAGACTATCAAGTTCATGTACACAGACTGGGCCGATAAGGAAAACCC  
GGAGACGCGGCGGAAAACCTGGTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCCGCGTGGCCGCGGACCT  
GCACGCGCAGTACGGCTCCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAATGAAGCCAGCTG  
GGCAGATTCCGCCCATGGTGATGAGGTCCCCTATGTCTTCCGCATCCCCATGATCGGTCCCACCGAGCTCTTCAG  
TTGTAACTTTTCCAAGAACGACGTGATGCTCAGCGCCGTGGTTCATGACCTACTGGACGAACTTCGCCAAAACCTGG  
TGATCCAAATCAACCAGTTCTCCTCAGGATACCAAGTTCAATTCACACAAAACCCAACCGCTTTGAAGAAGTGGCCTG  
GTCCAAGTATAATCCCAAAGACCAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGGGC  
AACGAAAGTGGCTTTCTGGTTGGAACCTGTTTCTCATTTGCACAACTTGAACGAGATATTCCAGTATGTTTCAAC  
AACCACAAAGGTTCTCCACCAGACATGACATCAATTCCTATGGCACCCCGCGATCTCCCGCCAAGATATGGCC  
AACCACAAACGCCCAGCAATCACTCCTGCCAACAATCCCAAACACTCTAAGGACCCCTACAAAACAGGGCCTGA  
GGACACAACGTCTCTCATTTGAAACCAAACGAGATTATTCACCCGAATTAAGTGTCAACATTGCCGTGGGGCGTC  
GCTCCTCTTCTCAACATCTTAGCTTTTGGCGGCTGTACTACAAAAGGACAAGAGGCGCCATGAGACTCACAG  
GCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCACATCCAGAACGAAGAGATCATGTCTCTGCAGAT  
GAAGCAGCTGGAACACGATCACGAGTGTGAGTCTGTCAGGCACACGACACTGAGGCTCACCTGCCCGCCAGA  
CTACACCTCAGCTGCGCCGGTCCGCGAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA  
CACACTGACGGGGATGCAGCCTTTGCACACTTTTAACACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA  
CGGACATTCCACCCTAGAGTATAGCTTTGGCCCTATTTCCCTTCTATCCCTCTGCCCTACCCGCTCAGCAACAT  
AGAAGAGGGAAGGAAAGAGAGAAAGGAAAGAGAGAGAGAGAAAGAAAGTCTCCAGACCAGGAATGTTTTTGTCCCCT  
GACTTAAGACAAAAATGCAAAAAGGCAGTCACTCCATCCCGGCAGACCCCTTATCGTTGGTGTTCCTCAGTATTAC  
AAGATCAACTTCTGACCCTGTGAAATGTGAGAAGTACACATTTCTGTTAAATAACTGCTTTAAGATCTCTACCA  
CTCCAATCAATGTTTAGTGTGATAGGACATCACCATTTCAAGCCCCGGGTGTTTCCAACGTCATGGAAGCAGCT  
GACACTTCTGAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGGAAGTTTAAACATTTCTTTCTGTGC  
CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGCCAGCACATGGAGCTGTAATCCAG  
AGAGAAGGAAACGTAGAAATTTATTATTAAGAATGGACTGTGCAGCGAAATCTGTACGGTTCTGTGCAAAGAG  
GTGTTTTGCCAGCCTGAACTATATTTAAGAGACTTTGT

09978192-101501

## **FIGURE 151**

MLNSNVLLWLTALAIAKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVYPYASP  
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPIWFTANLDTLMTYVQDQN  
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFFGGDPKR  
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCMNL  
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV  
NQGEGLKFVDGIVDNEGDVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIFMYTDWADKENP  
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEV PYV  
FGIPMIGPTTELFSCNFSKNDVMLS AVVM TYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMTS  
FPYGTRRSPAKIWPTTKRPAITPANNPKH SKDPHKTGPEDTTVLIETKRDYSTE LSVTI AVG  
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE  
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN  
LPHGHSTTRV

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domains:**

amino acids 189-204, 675-692

## FIGURE 152

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTTCGTGGCAGCAGTGGCGGCGATGTTTGT  
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCA  
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTCGAAGCC  
CTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA  
TGACCCAGTATATCCGCCTTACCCCAAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG  
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAAA  
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC  
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT  
GAGGAGAAGCAGCAAGAGCGGGTATTCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT  
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC  
GCAATCTTCATTACGACACCTTCTTGGTGAATTCGCTACGTCAAGAGGCATTTGACGATAATG  
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC  
CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
TTTCTTGAAGTTGTTTGAACGTGACAGTGGAGAGAACCCCAAGAGGAAAAGCTCCATCGA  
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC  
CCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTTCTCCCTGGTGTCTTCTGTATTTGCCA  
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA  
GCCCTCCTGCTGCCACCCTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCATG  
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG  
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTCCTATGGTTGTGCATGGGGACATCTAACT  
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC  
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC  
AGAATTTCATAGCCAGGCTGCCGTGTTGTTTGAAGTCTCAGAAGGCCCTTCTACTTCAGTTTTG  
AATCCACAAAGAATTAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTTCGTTGGGTT  
TTGCATTTGACCCAACCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAAACT  
TCTTCCCTGCCTTACCTTCTTTCACTCCATTCAATTGTCTCTCTGTGTGCAACCTGAGCTG  
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTTAC  
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT  
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG  
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCAATGTG  
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT  
TACGATTTTTTGAATCCCACTTTGAGTGTCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT  
GGGCTTGGATATTGCCCAAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT  
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT  
CACTGTCAATTGAGCAGCACAGCCTGAGTGTGGCCTCTGTCAACCCTTATTCCACTGCCTTA  
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG  
AGTCTCCTTGGAGGGCCTGGAACCTCTGAGTCTCCTATGAACCTCTGTAGCCTAAATGAAAT  
TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCG  
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

## **FIGURE 153**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPPQVAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLGMNAMVMTQYIRLTQDMQSKQALWNRVPCFLRDWELQVHFKEHGQKKN  
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSY  
DHERDGRPTTELGGCTAIVRNHLYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLPSVDNMKLPENTAPLPPLS  
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

**Signal sequence:**

amino acids 1-38

**Transmembrane domain:**

amino acids 310-329

## FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT  
CTGATGGTGGGTCGTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAGAAT  
TGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT  
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTTCCGCAACCGCTTCT  
TGCTGTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT  
CGACTCCTAAGAATGGAATGAGTAGCAAGAGCTCGAAAGAGAATCATGCCCGACCCTGTGACGAGCCCCCTGTGA  
CAGACCCCGTTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCTATGCCC  
CGCATCATTTTTAAGCTGGTCTCAGTGCAATGTGTTTCATTGCCCACGGAGACAGGTACCCACTGTATGTCATTCCCA  
AAACAAAGCGACCAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA  
TTAGTCACATGTCAAAGGATCCGGAGCCTCTTTGAAAGCCCTTGAACCTCCTTGCCCTCTTTACCCAAATCACC  
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGTGTGAGGGATA  
TCTATCTAAAGAAACACAAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCCTGGGAAAA  
GCCGGACCCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTCA  
GGCACCAGCCAAGTGCCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAACAGTATCTGGAAGAGGAGC  
AGCGTCGTAGTACCTCCTACGTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG  
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTCAGCT  
TTCCCTGTACAGAAATGGCTGTGTTGACATGGAGCATTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA  
GGGAAAGACGGGAGAAGAAATTGTACTTCGGGTATTCTCTCCTGGGTGCCACCCCATCCTGAACCAAACCATCG  
GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACCTCTGT  
CACCAGTTCTCAGTGCCTTGGGCCTTTTCAGAAGCCAGGTTCCCAAGGTTTGAGCCAGGTTGATCTTTGAGCTTT  
GGCAAGACAGAGAAAAGCCCAGTGAACATTCCTGCCGATTCTTTACAATGGCGTCGATGTACATTCACACCT  
CTTTCTGCCAAGACCACCAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAA  
GGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTACAGGGAAGGATTCTAAAGG  
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTGTCTGTTAC  
TAAGGTTAGAAGATTATTGCTTTTTTAAAGGCTAAATATTGTTTGTGGGAACCACAGATGGTTGGGGTTGAACAGT  
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT  
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC  
TCTTCTGGCCTGCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAATTTTTTTAATCTTAGACATT  
TTTACCTTGTCTTGTGAAGAATTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACCTTTTCTGTAAAGG  
GCCAGATTGTAAATATTTTCACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCTATACTACTCAACTCTGT  
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCAGGCCAGACAAAACA  
GATGGTGACCAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC  
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAAATTATTCAATGGTTCTCCAGTAACCTCTGCTAGAAACA  
CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA  
AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTTAAGTATGTTCTAAATATTTGT  
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAATATT  
TTCTAAGACCAGTTTTAGATGACTCTTATTCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG  
GAGGCTAGAAGATGAATTCAGGCACCTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA  
ACTGGATTCATTTTTAAACATTTTCATCAGTTTCAAATGGTAAATTCTGATTGATTTTTTAAATGCGTTTTTGGGA  
AGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG  
TGATTTCTGAACATAATGGTGCTAATTACAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTATCGGCATTCC  
AACTTTTTCTCTTTGTTTTTGTCCAGTGTGCAATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

## **FIGURE 155**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDVPY  
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDYPLYVIPKTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK  
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP  
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMMLCHFCHNVSFPC  
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLGGAHPILNQITGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSF  
CQDHHKRSPKPMCPLENLVRFVKRDMFVALGGSGTNYDACHREGF

**Signal sequence:**

amino acids 1-18

09978192-101501  
TOSTOT-26181660



AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCTTTTGAAGAACAGTACTGTGGA  
 GCTATTTAAGAGATAAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC  
 GCCGCTGTTACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGCACGCGCCTGAAGCACAAGCAGAT  
 AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTAT  
 GGGCGAAGGAAGTCTCCTGACTTCAGTGGTTAAGGGCAGAATGAAAATAATTCTGGGAGGAAGATAAGAATGAT  
 TCTGTGCGCGACTGCACCGGACTACAAAGGGCTGTCTCTGCTGGGAATCCTCTGGGACTCTGTGGGAGACCGG  
 ATGCACCCAGATACGCTATTTCAGTTCCCGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT  
 GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCAGAGGTAGGACGCAGCTTTTTCGCCCT  
 GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG  
 TCAATTAATCTAGACATTTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA  
 CGACAATGCCCTTACTTTCTGTGAAAGTGAATTAGAAATAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT  
 CCTCTACCCACAGCTTGGGATCCGGATCCGGAAGAACTCTGCGAGAGTACGAGCTCAGCCCCGAACACTCA  
 CTTTCTCCTCATCGTGCAAAATGGAGCCGACGGTAGTAGTAAGTACCCTGAATTTGGTGTGAAACGCGCCCTGGACCG  
 CGAAGAAAAGGCTGCTCACCACCTGGTCTTTACGGCTTCCGACGGGGGCGACCCGGTGGCGCACAGGCACCGCGCG  
 CATCCGCGTGATGGTTCTGGATGCGAACGACAACGCACCAGCGTTTGTCTCAGCCCGAGTACCGCGCGAGCGTTCC  
 GGAGAATCTGGCCTTGGGCACGCAGCTGCTTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT  
 GAGGTATTTCTTCCGGTATGTGGACGACAAGGCGGCCAAGTTTTCAAACCTAGATTGTAATTCAGGGACAATATC  
 AACATATAGGGGAGTTGGACCAAGGAGTCAAGATTCTACCAAGATGGAAGTGCAAGCAATGGATAATGCAGGATA  
 TTCTGCGCGAGCCAAAGTCTGTACTCTGTTCTGGACGTGAACGACAATGCCCAAGATGGTCTCTCACTCTCT  
 CGCCAGCTCGGTTCCCGAAAACCTCTCCAGAGGGACATTAAATGCCCCCTTTAAATGTAAATGACCAAGATTCTGA  
 GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAATCTTACGGAAATTACTA  
 TAGTTTAGTCAAGACATAGTCTTGGATAGGGAACAGGTTCTTAGCTACAACATCACAGTGACCGCCACTGACCG  
 GGGAACCCCGCCCCCTATCCACGGAAACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCCGGTCTT  
 CCTCTAGGCTCTCTAATCCGCTTATATCCAGAGAACAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA  
 CGACCCGACTGTGAAGGAAACGCCACGATCACTTATTCCTGGCTGAGAACACCATCAAGGGGCAAGCCTATC  
 GTCCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTCCGAGA  
 CTTGCAAGTGAAAGTGATGGCGCGGGACAACGGGCACCCGCCCTCAGCAGCAACGTGTCTGTTGAGCCTGTTCTG  
 GCTGGACGAGAACGACAATGCGCCCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTTCCACTGGCGTGGAGCT  
 GGCTCCCCGCTCCGCAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC  
 CTGGCTGTCTCAACGCTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG  
 CACGGCGGAGCCCTGTCTGACAGAGACCGGCTCAAGCAGAGCCCTCGTAGTGGCCGTCCAGGACCAAGCCGACG  
 CCTCTCTCCGCCACTGTCAAGCTCAGGCTGCCCCGTGGCCGACAGCATCCCCAAGTCTCTGGGACACTCCGACG  
 CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCGCGGTCTCCTG  
 CGTCTTCTGGCCTTCGTATCTTGTCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTACGCGCTGCTGCAGGC  
 TTCAGGAGGCGGCTTGACAGGAGCGCCGGCGTGCACATTGTGGGCGTGGACGGGGTGCAGGCTTTCTGCAGAC  
 CTATTTCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGAGTCACTTGATCTTCCCCCAGCCCAACTATGCAGA  
 CATGCTCGTCAAGCAGGAGGAGTTTGA AAAAAGAGCGCCCTTTTGTCTGTCAAGTGATTCGGTATTTTCTAAAGA  
 CAGTCTATGGGTTAATTGAGGTGAGTTTATATCAAACTCTTTCTTTTAAATTGCTCTGTCTCCGAAGC  
 TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCCTCAAACCTTCTAGGCTCAAGCAATTATCCACCTTTGCT  
 CCGGTGTAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCTAT  
 CTATCTATCTATCTATCTATTACTTTCTTGTACAGACGGGAGTCTCACGCCGTGTAATCCAGTACTTTGGGAGGC  
 CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGAAGACCAGCTGGAACCAACATGGAGAAACCCCGTCTATACTAA  
 AAAAATACAAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT  
 TGCTTTAACTCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG  
 AAACCTCTATCTCA

AAACTCTATCTCA

## **FIGURE 157**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAER  
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR  
DINDNAPYFRESELEIKISENAATEMRFP LPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA  
DGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR  
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE  
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVLTSLASSVPENSPRGTLIALLNVN  
DQDSEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLST  
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTI  
QGASLSSYVSINSDTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN  
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQNAWLSYRLLKASEPGLFSVG  
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPQVLADLGSLESPA  
NSETSDLTLYLVVAVAAVSCVFLAFVILL LALRLRRWHKSRL LQASGGGLTGAPASHFVGVD  
GVQAF LQTYSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL  
IEVSLYQIFFLFFFNC SVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRD YRCKPPTVCLS  
IYLSIYLSIYLSIYLLLSCTDGSLTPVIPVLWEAEAGGSPEVGSLRPA

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domains:**

amino acids 693-711, 809-823, 869-888

0978192-101501

## **FIGURE 158**

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG  
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGGTTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTT  
ACAGCTGCCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT  
CTGGTTC

## **FIGURE 159**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL  
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIHPHCYNSSDVEDHNHDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENF PDTLNCAEVKIFPQKKCED  
AYPGQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

### **Important Features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 51-71

#### **N-glycosylation site.**

amino acids 110-113

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

#### **Tyrosine kinase phosphorylation site.**

amino acids 182-188

#### **Kringle domain proteins motif**

amino acids 205-217

## FIGURE 160

GGCGCCGGTGACACGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCGC  
CGCGCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCGGGCCCGCGCCCCGC  
GCCCCGCGCCAGGTGAGCGCTCCGCCCCGCGGAGGCCCGCCCCGGGCCCGCCCCGCCCCG  
CCCCGGCCGGCGGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACCTGATCCCATAAAAC  
ATTTCATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCCCGCCCTCG  
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCCGGGGCCGGGCCGTAGCGGCGGCGCCTGGA  
TGCGGACCCGCGCCGCGGGGAGACGGGCGCCCCGCCGAAACGACTTTCAGTCCCCGACGCGC  
CCCGCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG  
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA  
GCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG  
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGC  
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
GGTCTGTGGACCTGCCACATTCCACGGCCTGGGCCGCTACACACGCTGCACCTGGACCGC  
TGCGGCCTGCAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA  
CACACCTCTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCCGAGCGCGCCTTCCGTGGGCTG  
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGCCCCATGTGCACCCGCATGCCTT  
CCGTGACCTTGGCCGCTCATGACACTCTATCTGTTTGCCAAACAATCTATCAGCGCTGCCCA  
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
TGTGACTGCCGGGCACGCCCCACTCTGGGCCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGA  
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG  
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC  
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT  
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG  
ACAGCCCGCCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCTTTGGGACTCTG  
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT  
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCAGCCACT  
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGAATCAGAAGGCTCAGGTGCC  
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT  
TGGGCCCTGCTGAACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC  
GGGGTCTCTCTCCACGCCGCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG  
GTCCTCCCTGATGGACGCTGCCGCCCCGCCACCCCATCTCCACCCCATCATGTTTACAGGG  
TTCGGCGGCAGCGTTTGTTCAGAACGCCGCTCCACCCAGATCGCGGTATATAGAGATAT  
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA  
AAAA

## **FIGURE 161**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI  
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAAF TGLALLEQLDLSDNAQLRSVDPA  
TFHGLGRLHTLHLDRCLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP  
LRALQYLRLNDNPWVCDRCRARPLWAWLQKFRGSSSEVP CSLPQRLAGRDLKRLAANDLQGCA  
VATGPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDSESGALPSLTCSLTPLGLALVLWTVLGPC

**Important features:**

**Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425

## FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC  
 TCACTGGCATATTTCTGAGGTATCTGTAGAATAACACAGCCTCAGATACTGGGGACTTTAC  
 AGTCCACAGAACCGTCCTCCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA  
 AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTTCTCTTTTGGGCTTATCTCTGGCG  
 GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCAC  
 CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGTTAGGGTTG  
 TTTCCAGAGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT  
 GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT  
 GTTGCTAGAGAGTCCCTTCGAGTTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
 ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG  
 ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
 TATAATCAGCCCCAACTCCTATTTTTCGGGTCTCACCCGCAAACGCAGTGATGGCAGGAAAT  
 ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA  
 CTCACAGCACTGGATGGTGGCTCTCCGCCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT  
 CCTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG  
 AGGACAGTCCGGTAGGCTTCTCGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC  
 AACGGAGAGATTTCTTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAACCTTTAAGAT  
 CAATCCCTTGACAGGAGAAATTGAACTAAAAAACAACCTCGATTTCGAAAACTTCAGTCCT  
 ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGAAAATGCACCGTTCTGATT  
 CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT  
 ACCTGAGAACGCGCCTGAAACTGTGGTTGCACTTTTCAGTGTTTCAGATCTTGATTACAGGAG  
 AAAATGGGAAAATTAGTTGCTCCATTACAGGAGGATCTACCCTTCTCCTGAAATCCGCGGAA  
 AACTTTTACACCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT  
 CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
 TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCCTGTTTCGTC  
 CGCGAGAACAACAGCCCCGCCCTGCACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG  
 CACCAACGCCCAGGTCACTACTCGCTGCTGCCGCCCCAGGACCCGCACCTGCCCTCACAT  
 CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCTCTGGACTACGAG  
 GCCCTGCAGGGGTTCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG  
 CGAGGCGCTGGTGCGCGTGGTGGTGGTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC  
 CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGCCGGGCTAC  
 CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCGTACCA  
 GCTGCTCAAGGCCACGGAGCTCGGTCTGTTTCGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA  
 CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGGTCAAGGAC  
 AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC  
 CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGACCCAGGCCAGGCCGACTTGCTCACCG  
 TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTT  
 GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCTCGGTGGGTGCTGCTTGGTGCCCGA  
 GGGCCCCCTTCCAGGGCATCTTGTTGGACATGAGCGGCACCGAGACCCTATCCAGAGCTACC  
 AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCTTGAAGCCGATT  
 ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA  
 TAACTTTGGGTTCAATATTCAGTGACCATAGTTGACTTTTACATTCCATAGGTATTTTATTT  
 TGTGGCATTTCCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT  
 TTACTCTTGATTTTTCTCATGTTCTTCTCCCTTGTGTTTAAAGTGAACATTTACCTTTATT  
 CCTGGTTCCT

## **FIGURE 163**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSLFLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR  
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTPCVLRQVLLLESPFEFFQAEQV  
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY  
RVQISEDSPVGFLVVKVSATDVDVTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS  
DLDSGENGKISCSIQEDLPFLLKSAENFYTLLTERPLDRESRAEYNITITVTDLGTPMLITQ  
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGFLGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA  
ADLLTVYLVVALASVSSLFVSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMMSGTRT  
LSQSYQYEVCLAGSGGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 685-712

**Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

**N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789



## **FIGURE 164**

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC  
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT  
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG  
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG  
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG  
TGATTCTTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG  
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG  
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT  
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT  
GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT  
CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC  
TGTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAACAGATC  
GAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT  
GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA  
CTGGTTGCTTGTATTTTCCTTATTCTTTTTAATTAGTTTTATTATGTATGCTACCATTGAA  
CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA  
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCAATAG

## **FIGURE 165**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE  
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC  
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE  
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFALDAS  
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETCLKIFIFNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSVDWLLVFSLSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domain:**

amino acids 321-340

#### **Homologous region to dilsufide isomerase**

amino acids 212-302

#### **N-glycosylation site.**

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296

#### **Thioredoxin domain**

amino acids 211-227

09978192-101501

## **FIGURE 166**

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGGGCTCTTCCTC  
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAAGTGAAGGACCGCTGCGCCCCGGTCATGTCCG  
CCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG  
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG  
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAAGTGCACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA  
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC  
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT  
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTTCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTTGTAAGAAATATTCAAACCTAATA  
AAATCATGAATATTTTAA

## **FIGURE 167**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHSLCVQVKDR  
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM  
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSEKDLKSVLWLKDSLQCTCE  
EMNDINAPYLVMGQKQGELVITSVKRWQKGQREFKRISRSIRKLQC

**Important features:**

**Signal peptide:**

amino acids 1-20

**Cysteine rich domain, homologous to frizzled N terminus**

amino acids 6-153

09978492-101501

## **FIGURE 168**

GTGGAGGCCGCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTGCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG  
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTGCGGGCTCCGTGCGGGCG  
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTGCAACCCTCTGGGCGTCCTTGTGGCCAATGTGCT  
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCGGTTAATGCTCGGTGTCTATACCATCC  
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCTG  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCCCTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA  
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG  
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCCAGCACGGCGACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGAGCCCCACCCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCACAGCACCAGCGCCCTCCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAAGTCCAGGTTGCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

09978192:101501

## **FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPVLV  
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCLEFSLACVPFALVSQLOGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GEGAATGMIFVLGQAEGILIMLMTALTVRREPSLSTCQQGEDPLDWTVSLLLMAGLCTFF  
SCILAVFFHTPYRRLQAESGEPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

### **Important features:**

#### **Signal peptide:**

amino acids 1-44

#### **Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

#### **N-glycosylation site.**

amino acids 40-43 and 43-46

#### **Glycosaminoglycan attachment site.**

amino acids 468-471

# FIGURE 170

GTCCACATCCTGCTCAACTGGGTGAGTCCCTCTTAGACCAGCTCTTGTCATCATTGCTGAAGTGGACCAAC  
TAGTTCCCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGGCCTTGCCCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG  
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTT  
TCTGAATCTAGCCCACTTGGCGGTAAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG  
CTACTTATTTCTTTTAGGGGATTGTGTCAGGAGGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC  
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACTGGGCCGGGAGGAGGCGGAGGCAAGCTGGGGCCGCCTT  
CCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGTCTAGCACAGGCAGGCG  
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTTGCCACAGGGGATTT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGAGCATCAATGACCACCAGCCACGGTTTCCCAAAGGCGAGCAGGA  
GCTGGAAATCTCTGAGAGCGCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCCC  
TAACACCCCTGCACACCTTCACTCTGTCTCCCAGTGAGCACTTGGCCTTGGATGTCAATTGTGGGCCCTGATGAGAC  
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCATTTTTTGATCTGGTGTAACTGC  
CTATGACAATGGGAACCCCCCAAGTCAAGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAG  
CCCTGCGTTTGTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT  
GACCGCCACAGACCCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCTCCAGAGGT  
GCTGGACACCTTCACTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTCGACCTCTAGACTATGAAAAGAACC  
TGCTTACGAGGTGGATGTTTCAAGCAAGGGACCTGGGTCCCAATCCTATCCAGCCCATTTGCAAAGTTCTCATCAA  
GGTTCTGGATGTCAATGACAACATCCAAGCATCCACGTCACATGGGCCCTCCAGCCATCACTGGTGTGAGAAGC  
TCTTCCCAAGGACAGTTTTTATTGCTCTTGTCTATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG  
CTGGCTGAGCCAGAGCTGGGCCACTTCAAGGTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC  
CACACTGGACAGAGAGCAGTGGCCCAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC  
AGCCAAGAAACAGCTCAGCATTGATGACATCAACGACAATGCACCTGTGTTTGAAGAAAGCAGGTATGA  
AGTCTCCACGCGGGAAACAACTTACCTCTCTTCACTTCACTTACCATCAAGGCTCATGATGCAGACTTGGGCAT  
TAATGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA  
GGTCACTGCTCAGAGGTCACTGAACTATGAAGAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCGG  
GCAACCCATGCTTGCATCCAGTGTCTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT  
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCCTCCACAGGCCACCTGCTGGTGCC  
CTTGAGACTCCCAATGGCTTGGGCCAGCGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT  
CCTTTTGACAACCAATTGTGGCAAGAGATGCGAGCTCGGGGCAATGGAGAGCCCTCTACAGCATCCGCAATGG  
AAATGAAGCCCACCTCTTCATCCTCAACCCTCATACGGGGCAGCTGTTTCTCAATGTACCAATGCCAGCAGCCT  
CATTTGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT  
GAGGGTCATGTTTGTACCAAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT  
GCTGACGGTGATCTGCTGGCTGTACTGTTGGGCATCTTGGGTTGATCCTGGCTTTGTTTATGTCCATCTGCCC  
GACAGAAAAGAAGCAACAGGGCTTACAGTGTGGGAGGCGGAGTCCACCTACCGCCAGGACCCCAAGAGGCC  
CCAGAAAACATTCAGAAGGCAGACATCCACCTCGTGCTGTGCTCAGGGGTGAGGAGGCTTGTGAACT  
CGGGCAGTCCCAAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCTT  
CCACCTCACCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGAGCACCGGCGGAGAGCCGAGAGGT  
GCTGCAAGACACGGTCAACCTCCTTTTCAACCATCCAGGCAGAGGAATGCCCTCCCGGAGAACCTGAACCTTCC  
CGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCTCTGAAGGTTGACAGGCAGCCCCACAGGGAGGCTGGC  
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACCGCCTCTCTGCAACCCTGAGACGGCAGCCGACATCT  
CAATGGCAAAGTGTCCCCTGAGAAAGAATCAGGGCCCCGTCAGATCCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC  
TGCCCTTCGCGGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTTCAAGCAATCTCCAGCTGCT  
GTCCTTGTGTCATCAGGGCCAATTCCAGCCCAAACCAAACCCAGGAAATAAGTACTTGGCCAAGCCAGGAGG  
CAGCAGGAGTGCAATCCCAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA  
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC  
CAGCACAGGTCTGGCCCTGGACCGCTGAGCGCCCTGACCCCGCTGGATGGCGAGACTCTCTTTGCCCTCAC  
CACCAACTACCGTGACAATGTGATCTCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTTCCG  
CAAGGCAGAGGCACAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT  
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCCTGGAGGCCGCTCCGAGGCGCTGCGGCGGCTCTCGGT  
CTGCGGGAGGACCTCAGTTTGAAGTGGCCACAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG  
AAAGACGGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGGAGGCTGCTGTAACATACCTCAGACGCCT  
CTGGATCCAAGAACCAGGGGCTGAGGATCTGTGGAACAGAGCTGGTTTCTAAAATCTTGTAACTCACTAGCTAG  
CGGCGGCTGAGAACTTTAGGGTGACTGATGATACCCCAAGAGGAGGCAAGAGCCCAAGGACTCAACAGCTGAC  
TGACCAAAGCAGCCCTTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGT  
TCCTGGCAAAACATATGTGGAGCACAAAGGGTCAGTCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG  
AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAAGGGGCTGTACCTGGGGGTGCCAGGAAATGCTCTCTGACCTAT  
CAATAAAGGAAAAGCAGTAAAAA

## **FIGURE 171**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA  
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQ  
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNLHTYTLSPSEHFALDVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESS  
LALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF  
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD  
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS  
YRIQDSPVAHLVAIDSNTGEVTAQRSLNYYEEMAGFEFQVIAEDSGQPMLASSVS VWVSL LDA  
NDNAPEVVQPVLS DGKASLSVLV NASTGHLLVPIETPNGLGPAGTDTPPLATHSSRPFLTT  
IVARDADSGANGEPLY SIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK  
KDNRAYNCREAESTYRQQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA  
GWDPCQLQAPFHLTPTLYRTL RNQGNQGAPAESREVLQDTVNLLFNHPRQRNASREN LNLPEP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVA AFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLA KP GGS  
RSAIPD TDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL  
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSDLATS AASGMKVQGDPPGGKTGTEGKSRGSS  
SSSRCL

### **Important features:**

#### **Signal peptide:**

amino acids 1-13

#### **Transmembrane domain:**

amino acids 719-739

#### **N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

#### **Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563



## FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTTCTCAGCCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAGTGACTCTC  
ATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT  
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG  
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT  
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCACAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT  
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTGCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA  
TACCGCACCATAACTACTGAAGTCCTTGGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT  
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC  
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTTCACTTCATAGCATACTCCTTCCCCGTCAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA  
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT  
AGGATTTCCGTTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAACAAAAAAGGGCGCGCGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

09978192.101501

## **FIGURE 173**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF  
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ  
QEVDAL EELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKEFFYAIS  
SKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## **FIGURE 174**

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA  
TCATGATTACCTCCCNGANACTATTTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT  
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT  
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT  
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT  
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT  
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

09978192-101501

## FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC  
TTTNTTGAATTCGGGGTTNNGNATACCTTCCCAGAAAATATTTTTTTGGATTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTTCATGGTGCCTTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN  
TAGGAGATCCCTTTCCCATTCTC

09978192-101501

# FIGURE 176

CTCGCGAGGGATCGTCCCATGCCGGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGATTTGCTACCTTTT  
TGGCTCCCTGCTCGTCAACTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCSCAA  
GGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG  
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGAGCAGGCGAATCGCACTGGAGGCCCTCTTCGCTTG  
CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA  
GGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATA  
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTCGCTGCTTTGTGCTCAGCCAGGA  
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCCAAGGCCATGAACAATT  
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCCCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC  
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGACGACGG  
TCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCGCCTCATCCCGGTCCCTGCCAACAGCTACTTTGGCTT  
CTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGGCCAACCA  
CAAGGGTGCTGTGGTCATCCTGCGCAAGGACAGCGCCAGTGCCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCG  
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGCTGGCCAGACCTGATAGTGGG  
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGCTGTGTATGTGTACTTTGAACCAGGGGGGTCACTG  
GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCTGGGATCAGCCTGGCTGTCTGGGGGA  
CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCTTTTGATGGTGATGGGAAAGTCTTCATCTACCA  
TGGGAGCAGCCTGGGGGTTGTGCGCAAACTTTCACAGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG  
CTACTCCCTGTCAGGCAGCTTGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACAC  
CGCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT  
GGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTTAGCTACATTGCAGTCCC  
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT  
TCCCCGTGTGACGTTCTTGAGCCGTAACTGGAAGAACCACAGCCCTCGGGCAGCTGGGCTGAAGCA  
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATTGT  
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGC  
CCCCATCCTCAATGCCCACCAGCCAGCACCCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGA  
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCACACC  
TCTGCCCATGGATGGATGGAAACAACAGCCCTGTTTGCACTGAGTGGGCAGCCAGTCATTGGCCTGGAGCTGAT  
GGTCACCAACCTGCCATCGGACCCAGCCAGCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTCCTGGT  
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCCTGCGGAGAAGCCACTCTGCCTGTCCAA  
TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTACCTTCTACCTCAT  
CCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCA  
GGAGCTGCATCCAGTCTCTGACGAGCCCGTGTCTTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC  
CCAGCAACTCTTCTTCTCTGGTGTGGTGAGGGGCGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGT  
CAAGTATGAGGTCCAGGTTTTCAACCAAGGCCAGTCGCTCAGAACCCCTGGGCTCTGCCCTTCTCAACATCATGTG  
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGG  
GCAGAAAGGGCTTTGCTCTCCAGGCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGCGGGA  
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGAGCGGCAGGAGCCCAGCATGTCTGGTGGCCAGTGTCTCTGC  
TGAGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAACTGTGTGGTGTTCAGCTGCCCACTCTA  
CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC  
TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACCTTGATGCTCCGAGA  
TGCTTCCACAGTGATCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGT  
CATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGCTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCTT  
CAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTTCGGGAAGACCGACAGCA  
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCCCCCGGCGGGAGGGCCCGGATGCACA  
CCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCTTAGGTTCC  
CATGTCCCAGCCTGGCCTGTGGCTGCCCTCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT  
GGGCTGCTGGTGTGCGATCAAGATTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCCACCCACAAGAAC  
TCCTCCCACCCAACTTCCCCTTAGAGTGTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG  
TGAGAAGGGCAGGGGTGTCCTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGT  
GTAACAGGACCCCAAGGACCTGCCCTCCCCGGAAGTGCCTTAACCTAGAGGGTCCGGGAGGAGGTTGTGTCACTGA  
CTCAGGCTGCTCCTTCTCTAGTTTCCCCTCTCATCTGACCTTAGTTTGTCTGCCATCAGTCTAGTGGTTTCGTGGT  
TTCGTCTATTTATTAAAAAATATTTGAGAACAAAAA

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## **FIGURE 177**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMOKESKENQWL  
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDGGEWKFC  
RPOGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVYVYLNQGGHWAGI  
SPLRLCGSPDSMFGISLAVLGD LNQDGF PDIAVGAPFDGDGKVFIYHGSSSLGVVAKPSQVLE  
GEAVGIKSFGYSLSGSLDMDGNQYPDLLVGSLADTAVLFRARPILHVSHEVSIAPRSIDLEQ  
PNCAGGHSVCVDLRVCF SYIAVPSSYSPTVALDYVLDADTD RRLRGQVPRVTFLSRNLEEPK  
HQASGT VWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTL SYSLQTPRLRRQAPGQGLPPVAP  
ILNAHQ PSTQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYSVGRALDPAEKPLCLSN  
ENASHVECELG NPMKRG AQVTFYLILSTSGIS IETTELEVELELLATISEQELHPVSARARVF  
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVT VSNQGQSLRTLGS AFLNIM  
WPHEIANGK WLLYPMQVELEGGQGPQKGLCS PRPNILHLDVDSRDRRRRELEPPEQQEPGE  
RQEPSMSWWPVSSAEKKKNITLDCARGTANC VVFSCLY SFDRAAVLHVWGRLWNSTFLEEY  
SAVKSLEVIVRANITVKSSIKNLMLRDASTVIPVMVYLDPM AVVAEGVPWWVILLAVLAGLL  
VLALLVLLLWKMGGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGS PRREGP  
DAHPIAADGHPELGPDPGHPGPGTA

### **Important features:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 1040-1062

#### **N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

#### **Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

## FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA  
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC  
TGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCGGAGACGAAGTAGAGGATGATTATTTCCGCACTTGAGTCCAGGAAAACCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATAATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTC AAGGCCCTTCATGAAAGTGGAA  
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAACTATGACCT  
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG  
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCATGGCAGTGTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGAGATTT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC  
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA  
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAAGTTTATGTTTAAAT  
AAGAATCATTGTGCTTTGAGTTTTTATATTCCTTACACAAAAGAAAATACATATGCAGTCTA  
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTACGAGAACAACTTTGT  
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG  
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAA

## **FIGURE 179**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPCP  
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLRPERSRFDTSILPI  
CKDSLGMFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSGVQCWCVDRYGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Leucine zipper pattern.**

amino acids 246-267

#### **N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

#### **Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352



## FIGURE 180

CAGACTCCAGATTTCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC  
CTCTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC  
GCTCTGCCTCCGGTGCTGCTGCCTGGGGCGGCCGGCTTACACCTTCCCTCGATAGCGACTTCACCTTTACCTT  
CCC GCCGCCAGAAGGAGTGCTTCTACAGCCCATGCCCCGTAAGGCCCTCGCTGGAGATCGAGTACCAAGTTTTA  
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCCTCTCCAGAAGGCAAAACCTTAGTTTTTTGAACAAAGAAAA  
TCAGATGGAGTTTACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTTCAGCACCATT  
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAG  
AAATATATTACTGGCACAGATATATTGGATATGAAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC  
AGACTAAGCAAAAAGTGGGCACATACAAATTCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGC  
AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCAATGGTGGTGGTGTGAGCCATTCAAGTTTTAT  
ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAACTAGAGTACGTAACATTGAAA  
AATGAGGCATAAAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAAATATTTTGAGATATA  
AAAGTAGGAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG  
TTGTACTTAAGTGTGTAACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATACTGCAT  
TTTCTAACTTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTTGGGCCTAATTGCAACACC  
AGTCTGTTTTTAACAGGTTCTATTACCCAGAACCTTTTTGTAAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT  
TCAGTTTTAAGTTATAAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCCA  
CTTTTCTCTATTACATATGCATCTCTCCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG  
AGATTTTTTATAACCAATACATTTTCAGTGTAAATATAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC  
CCAAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG  
AAATGAAGAATATAGTTTAAAAGCTTCTCCTCCATAGGGACACATTTTCTCTAACCCCTTAAGTAAAGTGTAGGA  
TTTTAAAATTAAGTGTGAGGTAAAATAAGTTTTATTTTAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA  
TAATCATGTTTATGTTAATTTTAACATGATTGCTGACTTGAGTAAAGTATTGATAATTTACCATGAGTTATGAAGGAAATA  
TTGCTAAAATGATCTGGGCCTACCATAAATAAATATCTCCTTTCTGAGCTTAAGAATTATCAGAAAAACAGGAA  
AGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAAATTCACTTAAGTAGAACTATAAATAAATATCTAGA  
ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG  
AACTTTGGCTGTAGGTTTTATTTTCTACAAGAATTCTGGTTTTGAATTATTTTTGTAAAGCAGGTACATTTTATA  
AAATGTAAGCCCTACTGTAAGTTTTAGCACTGGGTGTACATATTTATTAATAAATTTTTATTATAACAACCTTTTAT  
TAAAATGGCCCTTCTGAAACACTTTATTTTATTGATGTTGAAGTAAAGGATTAGAAACATAGACTCCCAAGTTTAA  
CACCTAAATGTGAATAACCCATATATACAACAAAGTTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC  
TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAATTTTAAAGTTATGCCCATTTATAACGTTGTTTTAT  
GACTACATTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT  
CTTGATGAGCAATAATGATAACCAGAGAGTGATTTCACTTACACTCATAGTAGTATAAAAAAGAGATACATTTCCC  
TCTTAGGCCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT  
ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA  
AGGTCAATAAGATCCTTGCCTATGAATACCCCTCCCTTTTGCCTGTATAAATTTGCAATGAGAAGCAAATTTACA  
GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAAGAATTCTA  
CCTCTCCTGTATGGCTGTACTGTACTGTACTCTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCT  
ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTTCAGTAACTTCTTACCATATAAAAAACGATAATTGCTT  
TATTTGAAAAGAATTTAGGAATACTAAGGACAATTATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG  
CATAACCAAAAAAGCAAACTTGTAAACAGAGTAAAAATCTTTAATATTTCTAAAGACATACTGTTTTATCTGCTT  
CATATGCTTTTTTTAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATGAGTAAGCTGTTTATCACTT  
AACAGCTCATTTTGTCTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTC  
CATAATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCCTAGAGTTTGCTCTGATATGCATTTGGATGATTAAT  
GTTATGCTGTTCTTTTATGTGAATGTCAAGACATGGAGGGTGTGTAATTTTATGGTAAAAATTAATCCTTCTTA  
CACATAATGGTGTCTTAAATTTGACAAAAATGAGCACTTACAATTGTATGTCTCTCAAATGAAGATTCTTTAT  
GTGAAATTTTAAAGACATTGATTCGCGCATGTAAGGATTTTTTCTGAAGTACAATAATGCACAATCAGTGTTG  
CTCAAAGTCTTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA  
AAATTATCAAAGGAAAA

## **FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLSDFTFTLPAGQKECFYQPMPLKASLEIEY  
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFEL  
ILDNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDN  
IQESNFDRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKSRT

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 195-217

#### **N-myristoylation site.**

amino acids 43-48

#### **Tyrosine kinase phosphorylation site.**

amino acids 55-62

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## **FIGURE 182**

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT  
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCTGGATG  
CTGCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAAGTACC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTACCAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG  
TAACAGCTACTCATACTGCTGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCCCTGGAAGAGAATATTCTCCCCAAACTGCCCTACCTGACTACCTTGTGATGATCCTCC  
TTCTTTTTCTTTTTCTTACCTTCATTTAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

09978192-101501

## **FIGURE 183**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM  
DADLACQKRPSGKLVSVLGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS  
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

**Important features:**

**Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

09978192.101501

## **FIGURE 184**

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC  
TGCTTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCGTGTCCTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

09978192.101501

## **FIGURE 185**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP  
FQGDSTVTKSCASKCKPSDVDGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

09978192 : 101501

## FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG  
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTC  
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT  
CTGATCAAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC  
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA  
GACACTTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC  
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTG  
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA  
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCAT  
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA  
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

## **FIGURE 187**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQOTIDNYQPYPCAEDDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWISKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ  
KDHHQASNSSRLHTCQRH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 256-259

#### **Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

09978192.101504



## **FIGURE 188**

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCTCGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGG

09978192-101501

## FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG  
CTGGGCCCGTCCGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA  
GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCATGGCAAGGTATATTTTTGTGGAATGAAAAGGA  
AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCT  
TGAAGTAATGTAGACAGAAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC  
TTAAATCAGAACTTGCATAAGAAAGAGAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG  
GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTGG  
AGTGTCCAAAACCTGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA  
AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA  
TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGACCTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
CTATTATCGTTATGATTTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC  
TGCTGTTAATTCTGGAGAACTGTGGTTTTGTAAATTTTTACTCCCCAGGCTGTTACACTGCCATCTTAAGCTCC  
CACATGGAGAGACTTTTGCTAAAGAAGTGGATGGGTACTTCAATTTGGAGCTGTTAACTGTGGTGTATGATAAT  
GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCATTTTTCGGTCTGGAATGGCCCCAGTGAAATA  
TCATGGAGACAGATCAAAGGAGAGTTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG  
GACAGGAAATTTTGTCAACTCCATACAACTGCTTTTGTGCTGCTGGTATTGGCTGGCTGATCACTTTTTTGTTCAAA  
AGGAGGAGATTGTTTGACTTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTGGATGCTAA  
AGAAATATATTTGGAAGTAATACATAATCTTCAGATTTTGAACACTCTTTCGGCAAAACACACTAGAGGATCGTTT  
GGCTCATCATCGGTGGCTGTTATTTTTTTCATTTTGGAAAAAATGAAATTCAAATGATCCTGAGCTGAAAAAAT  
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAAGTGTCTCTCTGCACCAGACATCTGTAGTAA  
TCTGTATGTTTTTTCAGCCGCTCTTAGCAGTATTTAAAGGACAAGGAACCAAGAAATATGAAATTCATCATGGAAA  
GAAGATTCTATATGATATACTTGCCCTTTGCCAAAGAAAGTGTGAATTTCTCATGTTACCACGCTTGGACCTCAAAA  
TTTTCTGCCAATGACAAAGAACCATGGCTTGTGATTCTTTGCCCCCTGGTGTCCACCATGTGAGCTTTTACT  
ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAAGTTTGGTACACTAGATTGTACAGTTTCATGA  
GGGACTCTGTAACATGTATAACATTCAAGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTTCATGAGTA  
TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC  
ACCCACCACCTTCAACGAACTAGTTACACAAAGAAAAACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG  
GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAAGAATGGCCCCGACATTAAGTGGACTGATCAACGTGGG  
CAGTATAGATTGCCAACAGTATCATTCTTTTTGTGCCCAGGAAAACGTTCAAAGATACCCCTGAGATAAGATTTTTT  
TCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGATGCTTATTCCCTGAGAAT  
CTGGGGTCTAGGATTTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTTCAAGTAAAAAGTTCTACAAGG  
GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCT  
CTTGGCTAGGATGATTAAAGGAAAAAGTGAAGCTGGAAAAGTAGACTGTGAGGCTTATGCTCAGACATGCCAGAA  
AGCTGGGATCAGGGCCTATCCAAGTGTAAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTCAAGAAGAGCA  
GATAAATACCAGAGATGCAAAAGCAATCGCTGCCCTTAATAAGTGAAAAAATGGAAACTCTCCGAAATCAAGGCAA  
GAGGAATAAGGATGAACCTTTGATAATGTTGAAGATGAAGAAAAAGTTTAAAGAAATTTCTGACAGATGACATCAG  
AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA  
GAATTATCTACAGCACTGGTGTAAAAGAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA  
GACTTTGCAGGCTATAATATATGGTTTCACACATGAGAACAAAGATAGAGTCATCATGTATTCTTTGTTATTTGCT  
TTTAAACAACCTTTAAAAAATATTAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCAAGTCCATG  
GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT  
ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTTCAGTTTTTTGGCTGACCTGAAAAGAGGTAAT  
TAGTTTTTGGTCACTTGTCTCTTAAAAATGCTATCCCTAACCATATATTTATATTTCTGTTTTAAAAACACCCAT  
GATGTGGCACAGTAAACAAACCTGTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTCTCTCTCA  
AAGGTTGAAAAAATGCTTTTAAATTTTTTCACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC  
AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTGTATCATCCAGGAAAACCTGAGGGGAAAAAATTA  
TAGCAATTAACCTGGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA  
TGTGTTTCATGTATTTTCTGAAATTGCTTTTCATAGAAATTTTCCACTGATAGTTGATTTTTGAGGCATCTAATAT  
TTACATATTTGCCTTCTGAACCTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTTTTCTTTTCATAGTTTTGG  
TTTTTCACTCCTGTCCAGTCTATTATTTATTTCAAATAGGAAAAATTACTTTACAGGTTGTTTTACTGTAGCTTAT  
AATGATACTGTAGTTATTTCCAGTTACTAGTTTACTGTGTCAGAGGGCTGCCTTTTTTCAGATAAATATTTGACATAATA  
ACTGAAGTTATTTTTATAAGAAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTTAGA  
CTCAAAGTAATCACAAATTTGTCAAGTAACATGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAATGGTAAAAAT  
CCAATCAGTCAAAGAGGTCAATGAATTAAGGCTTGCACTTTTTTCAAAAAAAAAAAAAAAAAA

## **FIGURE 190**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRD LKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL  
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLLEDNQGGQYESWNYRYDFGI  
YDDDPEIITLERREFDAAVNSGELWVFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS  
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN  
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP  
SLAVFKGQGTKYEYIHHGKKILYDILAFAKESVNSHVTTLGPQNFNPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEHEYEGHHS  
AEQILEFIEDLMNP SVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSRLIWGLG  
FLPQVSTD LTPQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDC  
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLET LRNQGRNKDEL

### **Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

## FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGGA  
GTCGTTGGTGAAGTTTTTTCATTCTCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCCTTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT  
GGGAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCACCA  
AAAATCCAAGCACAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCATCGTATATCAATATCTTTCTGAG  
ACTACAGAAGTTTTCTTCCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAAATAAATAAGCTCCAGCCAGAGATG  
TATGCATGATAATGATATGAATAGTTTTCGAATCAATGCTGCAAAGCTTTATTTTACATTTTTT  
TCAGTCCTGATAATATTAAAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCCCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCCCTT  
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT  
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT  
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTAAGATTGAGCATTGAAAGATTTCCCTAGCCTCTTCCCTTTT  
TCATTAGCCCAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAGTGACCCCTCTATATTTCCCTCCCTTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT  
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA  
CAATGGACCCAAGAGAAGAA

09978192-101501

## **FIGURE 192**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI  
LVLWDINKRGVEETAAECKRLGVTAHAYVVDSCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV  
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC  
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSLID  
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

#### **Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

09978192.101501

## **FIGURE 193**

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCAGCCCGCCGGGGC  
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTTCGGTGTTTCATGATCCT  
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACGTCCTTCT  
CTAGGCCGCACACGGGGCCGCGCTGCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACG  
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA  
CGTGACACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT  
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTTCTTCGTGCGCGACCCC  
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC  
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA  
CCCGTGCCAGATCGACTACGACTTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC  
GAGACTGAAAGCTTTCGCGTTGCTTTTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCC  
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

## **FIGURE 194**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSMILLIIVYWDSAGAAHFYLHTSF SRPHTGPPLPTPGPDRDRELT  
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFPTKERAFDDIPNSEL SHLIVDDRHGAIYCYVPKVACTNWK RVMIVLS  
GSL LHRGAPYRDPLRIPREHVHNASAHLT FNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLET LDEDAAQLLQLLQVDRQLRFPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLF GYPKPENLLRD

### **Important features:**

#### **Signal peptide:**

amino acids 1-31

#### **N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

#### **TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

## FIGURE 195

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCCTGGTTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA  
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG  
CCTACTGGGCCGCATGGGCCAGCCCGCTGAGGTCGGGGCTGCGGCAGTGTTCTTGGCCTCCGA  
AGCCAACCTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCAGAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCCCGATATCCCTTCCTGATTTCTCTCATTT  
CTACTTGGGGCCCCCTTCCTAGGACTCTCCACCCCAAACCTCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTCAACCTGCAGGTTCCCAT  
AAAAACGATTTGCAGCC

09978192-101501



## **FIGURE 196**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVVTGGGRGIGAGIVRAVNSGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPQRPPEETSAQGFRQLLELNLLGTYTLTKL  
ALPYLRKSQGNVINISLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAVFLASEANFCTGIELLVTGG  
AELGYGCKASRSTPVDAPDIPS

**Important features:**

**N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

## **FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATTGGACTGGCCTCACAACCTG  
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC  
TGGTGTACGGATGAAACCGTATGCCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCTGTGCGCCGCCG  
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA  
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG

09978192-101501  
T05T07-26T8X660

## **FIGURE 198**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGY SINHDPSRIPVDLPEARCLCL  
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETI AVGCTCIF

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

09978192-101501

## FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG  
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGAT  
CGCGGCTGTGGCGGCGACGGCAGGCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG  
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT  
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAAGAA  
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCAATTCAAGAACCAGGTTTGAGTG  
GCCGCTTCTTTGTCACTCTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT  
TATCGTGGCCCGAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC  
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGGAATT  
CCTGCTTGGTGTTCTTATGTGTTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAAAACAAAGACAGCCTTGATAGATGATGAAGAAGA  
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTTGGCTG  
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC  
TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC  
TGTAGATTTAATGATGCGTTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG  
CCTGCAGTTTGTACCAAATCCTTAATTTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCT  
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT  
GACAATCAGGATATAGAAAAACAAACGTAGTGTTGGGATCTGTTTGGAGACTGGGATGGGAA  
CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATC  
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT  
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCATCCTTTTCTTGTGTAAAGTATTTAT  
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGATGAAAAATCTTTCACAGCTAGAA  
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG  
TGCTATGTTTTATTTCTTACCTTTAATTTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT  
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT  
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAAAAAAATTGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTTT  
AAGTTTTCTAAGCAATATTTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT  
CTTGTGAAGAAAAGTTGAATACTGTTTTGTGTTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC  
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCTTTCAGTGATGTGCTTTTGGTGAAA  
GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTTGATTTTTGTTTCCATCTTCTGTAAATC  
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG  
GCTAATTTCTTT

## **FIGURE 200**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP  
WCPSCQQT DSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG  
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISECFYVPLPRHLSERSEQNRRSEEAHRAEQ LQDAEEEEK  
DDSNEEENKDSLVDDEEEKEDLGDEDEAE EEEEEEDNLAAGVDEERSEANDQGPPGEDGV TRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domain:**

amino acids 191-211

#### **N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

#### **Flavodoxin proteins**

amino acids 173-187

09978192-101504

## FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTAAACTCCGGTAAGTACCTAGCCCACATGATT  
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC  
CAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAATGGAATATCATCCTGATTTAGAAAAT  
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT  
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG  
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCC  
AGCCCTTGTCTCTCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCCT  
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG  
ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT  
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT  
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG  
TATGGATTACGTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT  
GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA  
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG  
TTTAGAGAGCTTGGCCAACCTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT  
GTATTTGTGACCTACAGGTAGGCTAGTATTATTTTTCTAGTTAGTAGATCCCTAGACATGG  
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTATTTTTTTGAGATAGGGTCT  
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC  
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTTGGTG  
TTTTTTGTAGAGACTGGGTTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG  
TGATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC  
CCCAAGCTTGAATTTTTATTCTGCCATTGACTTGGCATTTACCTTGGGTAAAGCCATAAGCGA  
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT  
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT  
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT  
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA  
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT  
TTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTTGCCAGGCTGGAGTGCAACGG  
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT  
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTTAGT  
AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC  
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT  
TGTATAATATGTAATTGTAGGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA  
AAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA  
ACAAGTATTAACATTTTGGGAATATGTTTTATTAGTTTTTGTGATGTACTGTTTTACAATTTTT  
ACCATTTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG  
TGCTGATTTGTCTTATTTTTTTTCACTTTTCCCACTGGTGCTATTTTTTATTTCCAATGGATA  
TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAAATATGTGAAAAGAAAT  
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTGGATTTTAT  
TTCAATAAAAAAAACTCTTATCAAAAAA

## **FIGURE 202**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 45-65

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

#### **N-myristoylation sites.**

amino acids 35-40 and 151-156

#### **Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

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# FIGURE 203

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCAGACCTGGAGGGTCTCGCTCTGTCA  
CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATGCC  
TCAGCCTCCCAGTAGCTGGGATTACAGGTGGTGACTTCCAAGAGTGACTCCGTGGAGGAAAATGACTCCCCAG  
TCGTGCTGCAGACGACACTGTTCTGTGAGTCTGCTCTTCTGGTCCAAGGTGCCCCACGGCAGGGGCCACAGG  
GAAGACTTTTCGCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGACCTG  
CGCATCTCCATCGAGAACTCCGAAGAGGGCCCTCACAGTCCATGCCCTTTTCCCTGCAGCCCACCTGCTTCCCGA  
TCCTTCCCTGACCCAGGGGCCCTTACCACCTTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACATCTTCTC  
TATGGCAAGCGTGACTTCTTGTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTG  
GCTCAGGGCCCCCGCTGTTAGCCACTTCTGTACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCC  
GCCAGCTTACCTTCTCCTTCCACAGTCTTCCCCACAGGCCGCTCACAATGCCTCGGTGGACATGTGCGAGCTC  
AAAAGGGACCTCCAGCTGCTCAGCCAGTTCCTGAAGCATCCCCAGAAGGCCTCAAGGAGGCCCTCGGCTGCCCTC  
GCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTGTGAGATTATGGGGGACATGGTGTCTTTCGAG  
GAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGG  
CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGC  
CGGAGCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCCAGCAGCCAAGCCCTGTTCCAGGACAAGAAATTC  
AGCCAAGTCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGTAGCCAACCTCACGGAGCCCGTG  
GTGCTCACTTTCCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCTGGGTTGAAGACCCCA  
TTGAGCAGCCCGGGCATTGGAGCAGTGTGGGTGTGAGACCGTCAGGAGAGAAACCAAACATCCTGCTTCTGC  
AACCCTTGACCTACTTTGCAGTGTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGC  
CTCCTCTCCTACGTGGGCTGTGTGCTCTTGCCTTGGCCTGCCTTGTACCATTGCGCCTACCTCTGCTCCAGG  
GTGCCCTTGGCGTGAGGAGGAAACCTCGGGACTACACCATCAAGGTGCACATGAACCTGCTGCTGGCCGTCTTC  
CTGCTGGACACGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCC  
ATCTTCTGCACTTCTCCCTGCTCACCTGCCCTTTCCTGGATGGGCCCTCGAGGGGTACAACCTCTACCGACTCTG  
GTGGAGGTCTTTGGACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTT  
CTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACCTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAG  
GGCGTCATCTACCTTCCATGTGCTGGATCCGGGACTCCCTGGTGCAGTACATACCAACCTGGGCCTCTTCAGC  
CTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGCAGATCCTGCGGCTGCGCCCCCACACCCAA  
AAGTGGTCACATGTGCTGACACTGCTGGGCCTCAGCCTGGTCCCTTGGCCTGCCCTGGGCCTTGATCTTCTTCTCC  
TTTGTCTTGGCACCTTCCAGCTTGTGCTCCTCTACCTTTTCAGCATCATCACCTCCTTCCAAGGCTTCCCTCATC  
TTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCTCCCTCTGAAGAGCAACTCAGACAGCGCC  
AGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTAGGCCTCCAGCCCACCTGCCCATGTGATGAAG  
CAGAGATGCGGCCTCGTCGCACACTGCCTGTGGCCCCCGAGCCAGGCCCAGCCCCAGGCCAGTCAGCCGCAGACT  
TTGGAAGCCCAACGACCATGGAGAGATGGGCCGTGGCCATGGTGGACGGACTCCCGGGCTGGGCTTTTGAATTG  
GCCTTGGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTAGGGTACTG  
TCCCCACATCTGTCCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTGGGCCAGCCCTCATTGCTGGG  
GGCCAGGCCTTGGATCTTGAAGGTCTGGCACATCCTTAATCCTGTGCCCTGCCTGGGACAGAAATGTGGCTCCA  
GTTGCTCTGTCTCTCGTGGTCACCTGAGGGCACTCTGCATCCTCTGTATTTTAACCTCAGGTGGCACCCAGGG  
CGAATGGGGCCCAGGGCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGC  
AGCTCGCCTACCTCTGAGCCAGGCCCTCCCTCCCTCAGCCCCCAGTCTCCTCCCTCATCTTCCCTGGGGTTC  
TCCTCCTCTCCAGGGCCTCCTTGTCTCTTCTGTTACAGCTGGGGGTCCCCGATTCCAATGCTGTTTTTTGGGGA  
GTGGTTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGTTTGTCTACTGCACAAGCCTCGGCCTGCCCTGAGCCA  
GGCTCGGTACCGATGCGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCCTTGTATGAGCTGCATTGCCCTTG  
CTCACCTGACCAAGCACACGCCTCAGAGGGGGCCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAACTGTGGA  
CCATGCCAGTCCCGTCTGGTTTCCATCCCACTCCAAGGACTGAGACTGACCTCCTCTGGTGACACTGGCCTA  
GAGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCCATCATGGT  
TAATTCTGTCCAACAAACACACAGGGTAGATTGCTGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTG  
GTCACCTCTCTGCCAATTCAGTCTGGTATGTGAGGCGTGCCTGAAGCAAGAACTCCTGGAGCTACAGGGACA  
GGGAGCCATCATTCCTGCCTGGGAATCCTGGAAGACTTCTGTCAGGAGTCAGCGTTCAATCTTGACCTTGAAGAT  
GGGAAGGATGTTCTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAGAAAGTACATGTTTATTGTAGAGA  
ATTTGGAAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAAATCAGCTGTTGTAATCGCCTAGCAAAAAAAAAAAAA  
AA



## **FIGURE 204**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRCSQRNQTHRSSLHYKPTPDLRISIENSE  
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPHTAAHNASVDMCELKRDLQLL  
SQFLKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTLQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANLTEPVVLTTFQHQLQPKNVTLQCVFWVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVVSALACLVTIAAYLCSRVPPLPC  
RRKPRDYTIKVHNMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE  
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY  
PSMCWIRDSLVSYITNLGLFSLVFLFNAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLG  
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLP  
ISSGSTSSSRI

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

#### **Microbodies C-terminal targeting signal.**

amino acids 691-693

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

#### **N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

#### **G-protein coupled receptors family 2 proteins**

amino acids 475-504

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## **FIGURE 205**

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACCTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTCTTCTGTTCAACATGG

09978192-101504

## FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCCAGGTTTTGCTTTGA  
TCCTTTTCAAAAACCTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCCT  
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGAC  
TCGGGAGTGGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTGCAGCAAATGAGCCTCTTCGGGC  
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTC  
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG  
GAAGTATTCACAGCCCCAAGGTTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG  
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT  
TCTGCATCCACTACAACATTGTTCATGCCACAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTT  
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTAGTACCTTGGGAAGACCTTATTCGATATCTTGAACCAG  
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTTGTTTTTGGAA  
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCT  
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCAGTACCATTTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG  
GTGGGAACCTGTGCCTGTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC  
ACGAGGTCCTTCAGTTGAGACCAAGACCGGTGTGAGGGGATGCAACAATCACTACCCGACGTGGCCCTGGAGC  
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA  
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTGCT  
TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA  
ACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAAGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTAT  
TAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTTTCAGTTCTTTTC  
GATACGGCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC  
TCTAAAGCTCCATGTCTCTGGGCCTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACAT  
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTTGCTATGAATTAACTTGT  
GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACA  
TTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTG  
TTTCATTGTGTACATTTTATATTCTCTTTTGTACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT  
ATTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACCTAGATCAACTATTTTTAGCTTGGTAAATTTTTCT  
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA  
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA  
GACTTTTTGAAAAATAATTAAATTATCATATCTTCATTCTGTATTGAGATGAAAATAAAAAGCAACTTATGA  
AAGTAGACATTGAGATCCAGCCATTACTAACCTATTCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT  
AAAGCACCTTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTA  
TTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTATGTACA  
GAAGTATGTCTCTTAACCAGTTCACCTATTGTACTCTGGCAATTTAAAAAGAAAATCAGTAAATATTTTTGCTTGT  
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAGA  
ATGTGGCTATTTTGGGGAGAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

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## **FIGURE 207**

MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNNLLTEEVRLY  
SCTPRNFSVSIREELEKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ  
LRPKTGVRGLHKSLTDVALEHHEECDVCRCGSTGG

**Signal sequence:**

amino acids 1-14

# FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGGAAGA  
 AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATTCTTATCCTTTTTTAACATAATCCTAATTTCC  
 AAATCCTTGGGGCTAGATGGTTCCTAACTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG  
 ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATTCCCACGAACACCACGAACCTCACCCCTC  
 ACCATTAACCACATAACCAGACATCTCCCCAGCGTCTCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTTCAGA  
 TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC  
 TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCCG  
 CCTAGCTTACAGCTTCTCAGCCTTGAGGGCCAACAACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC  
 AACATAGAAATACTCTACCTGGGCCAAAACGTGTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA  
 GATGCCCTTCTAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCCTACTGTT  
 TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC  
 CTCAACCAATTACAAATCTTGACCTAAGTGGAAATGGCCCTCGTTGTTATAATGCCCCATTTCTTGTCGCCCG  
 TGTAAAAATAATTCTCCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAGGTTTTACGTCTA  
 CACAGTAACCTCTCTCAGCATGTGCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC  
 CAAAACCTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAATTGGATCTG  
 TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG  
 AAAATCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA  
 AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGA  
 CTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT  
 GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCCTGGAACAATTACATTATTTTCAATATGATAAGTATGCA  
 AGGAGTTGCAGATTCAAAAACAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC  
 TTGGATCTAAGTAAAAATAGTATATTTTTCAGTCTCTGATTTTCAGCATCTTTCTTCTCAAATGCCTG  
 AATCTGTGAGGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATTTCAAACCTTTAGCAGAGCTGAGATATTG  
 GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT  
 ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT  
 CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA  
 ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG  
 AATCTGCTAAAAATTAGAGGAATTAGACATCTCTAAAAATTCCTAAGTTTCTTGCCCTTCTGGAGTTTTTGATGGT  
 ATGCCCTCCAAATCTAAAGAATCTCTCTTGGCCAAAAATGGGCTCAAATCTTTTCAAGTTGGAAGAACTCCAGTGT  
 CTAAGAACCTGGAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAAGTGTCC  
 AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC  
 CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTC  
 AACATCTGAAGATGTTGCTTTTGATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG  
 GTTAACCATACCGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC  
 CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA  
 TCTGTATCTCTCTTCTCATGGTGTGATGACAGCAAGTCACTCTATTTCTGGGATGTGTGGTATATTTACCAT  
 TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT  
 GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAA  
 CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAACCTTTCCAGAGCATA  
 CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAGATAGCATTTTAC  
 TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAGAAG  
 TCCAAGTTCCTCCAGCTCCGGAAGGCTCTGTGGGAGTTCTGTCTTGAGTGGCCAACAACCCGCAAGCTCAC  
 CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA  
 ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

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## **FIGURE 209**

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG  
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLQNCYYR  
NPCYVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF  
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL  
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ  
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH  
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLOKLMMNDNDISSSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSLFLPSGVFDGMPPNLKNLSL  
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDVWFVWVWNHTEVTIP  
YLATDVTCVGPGAHKQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLCLEE  
RDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 840-860

## FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAAACAGAAACATGGAAAACATGTTCCCTTC  
AGTCGTCAATGCTGACCTGCATTTTCTGCTAATATCTGGTTCCTGTGAGTTATGCGCCGAAGAAAAATTTTCTA  
GAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGCAGAGTGCAGCAATCGTCCGACTACAGGAAG  
TTCCCCAAACGGTGGGCAAATATGTGACAGAACTAGACCTGTCTGATAATTTATCACACACATAACGAATGAAT  
CATTTCAAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAAATC  
CCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCCCTCAACCTAAAAAACCTAAGGGAGTTACTGC  
TTGAAGACAACCAGTTACCCCAAATACCCCTCTGGTTTGCCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAACA  
ATATATACAACATAACTAAAGAGGGCATTTCAGACTTATAAACTTGAAAAATCTCTATTGGCCCTGGAAGTGCCT  
ATTTTAACAAAGTTTGGCGAGAAAACCTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT  
CACTATCTTTCAATTCTCTTTACACAGTGCCACCCAACTGCCAAGCTCCCTACGCAAACTTTTTCTGAGCAACA  
CCCAGTCAAATACATAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTACTAGATTTAAGCGGGAACT  
GTCCGAGGTGCTTCAATGCCCAATTTCCATGCGTGCCTTGTGATGGTGGTGGTCAATTAATATAGATCGTTTTG  
CTTTTCAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTATGCTGCCTGGT  
TTAAAAATATGCCTCATCTGAAGGTGCTGGATCTTGAATCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCAT  
TTTTAACGATGCTGCCCCGCTTAGAAATACCTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATCCACAGCATA  
TTAATATTTCCAGAACTTCTCTAAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTATGTGTTCCAGGAAC  
TCAGAGAAGATGATTTCCAGCCCCGTGATGCAGCTTCCAACTTATCGACTATCAACTTGGGTATTAATTTTATTA  
AGCAAATCGATTTCAAACTTTTCCAAAATTTCTCCAATCTGGAAATTATTTACTTGTGAGAAAACAGAAATATCAC  
CGTTGGTAAAGATACCCGGCAGAGTTATGCAATAGTTCTCTTTTCAACGTCAATATCCGGAACGACGCTCAA  
CAGATTTTGAGTTTGACCCACATTCGAACTTTTATCATTTTCAACCGTCTTTTAAATAAGCCACAATGTGCTGCTT  
ATGGAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCAAACCAATTTGAAAATCTTCTGACA  
TTGCCTGTTTAAATCTGTCTGCAAAATAGCAATGCTCAAGTGTTAAGTGGAACTGAATTTTCAGCCATTCCTCATG  
TCAAATATTTGGATTTGACAAACAATAGACTAGACTTTGATAATGCTAGTGCTCTTACTGAATGTCCGACTTGG  
AAGTTCTAGATCTCAGCTATAATTCACACTATTTCAGAATAGCAGGCGTAACACATCATCTAGAAATTTATTCAA  
ATTTCACAAATCTAAAGTTTAACTTGAGCCACAACAACATTTATACTTTAACAGATAAGTATAACCTGGAAA  
GCAAGTCCCTGGTAGAATTAGTTTTAGTGGCAATCGCCTTGACATTTTGTGGAATGATGATGACAACAGGTATA  
TCTCCATTTTCAAAGGTCTCAAGAACTGACACGTCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATG  
AAGCATTCCTTAATTTGCCAGCGAGTCTCACTGAACATACATAAATGATAATATGTTAAAGTTTTTTAACTGGA  
CACTACTCCAGAGTTTCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTACATAGAGC  
TATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCACCTACCCTCTGGCTTTC  
TTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAATCTGCTAAAAACAATCAACAAATCCGCACTTG  
AACTAAGACCACCACCAAATTAATCTATGTTGGAACACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAG  
ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAATTTCCAGACTGGTAGATGTCATTTGTGCCAGTCCCTG  
GGGATCAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACAACTTGTGTTTTCAGATGTCAGTGCAGTGATATTAT  
TTTTCTTCACGTTCTTTATCACCAACCATGGTTATGTTGGCTGCCCTGGCTCACCATTGTTTACTGGGATGTTT  
GGTTTATATATAATGTTGTTTGTAGCTAAGGTAAAAGGCTACAGGTCTCTTTCCACATCCCAAACCTTTCTATGATG  
CTTACATTTCTTATGACACCAAAGATGCCCTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAG  
AGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACC  
TCATGCAGAGCATCAACCAAAGCAAGAAAACAGTATTTGTTTTAACCAAAAAATATGAAAAAGCTGGAACTTTA  
AAACAGCTTTTTTACTTGGCTTTGCGAGGGCTAATGGATGAGAACATGGATGTGATTATATTTATCCTGCTGGAGC  
CAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACA  
ACCCGAAGGCAGAAGGCTTGTGTTTGGCAAACCTCTGAGAAATGTGGTCTTGACTGAAAAATGATTACCGGTATAACA  
ATATGTATGTCGATTCCATTAAGCAATACTAACTGACGTTAAGTCATGATTTGCGGCCATAATAAAGATGCAAAG  
GAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTATCCAAAACCTTAGTGGTTTAAACAACACA  
TTTGCTGGCCCAAGTTTTGGAGGTCAGGAGTCCAGGCCAGCATAACTGGGTCTCTGCTCAGGGTGTCTCAG  
AGGCTGCAATGTAGGTGTTCAACAGAGACATAGGCATCACTGGGGTCACACTCATGTGGTTGTTTTCTGGATTCA  
ATTCCTCCTGGGCTATTGGCCAAAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCCAAGGCAGCTTGCTTC  
ATCAGAGCTAGCAAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAAATCGAATCAAAAAAGTGAT  
ATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCACCAGCTCCATGGGAGTGACCACC  
TCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGATTGCTTCAGTTGGTCATCAACTATTTTCCCT  
TGACTGCTGTCTGGGATGGCCTGCTATCTTGATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACC  
ATCTTAGCAGTTGACCTAACACATCTTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCTTAATA  
TTAAGCTGTTGTTTATATTTATCATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTTCGGTTTTAT  
TTACAGTTGCTTTTACAAATATTTGCTGTAAACATTTGACTTCTAAGGTTTAGATGCCATTTAAGAACTGAGATGG  
ATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAGTATGCAGCTAAATTCGAAGCTTTTGGTCTATA  
TTGTTAATTGCCATTGCTGTAAATCTTAAATGAATGAATAAAATGTTTCATTTTACAAAAA

## FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPCDEKKQNDSVIAECSNRRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL  
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL  
TLDDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNLTLQLRYLNLSSTSLRKINAAWFKNM  
PHLKVLDLEFNLYVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL  
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLQNFNSNLEIIYLSENRISPLV  
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACNLNSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDELEV  
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFLNLPASLTEHINDNMLKFFNWT  
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHLDL  
SNLLKTINKSALETKTTHKLSMLELHGPNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQTIFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAII  
NMQSINQSKKTVFVLTKKYAKSWNFKTAFYLALQRLMDENMDVIIIFILLEPVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGLEFWQTLRNVVLTEENDSRYNMYVDSIKQY

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 826-848



## FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT  
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA  
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA  
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG  
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC  
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC  
TGGTGCACCTCCTTCCAGCAGCTCGGCGGCATCGACTCCCTGAGCGAGCAGATTCCTTCCTG  
GAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTG  
GACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC  
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG  
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG  
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTGA  
AAGGGCGGCCGCGACTCTAGAGT  
CGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTACAAAT

## **FIGURE 213**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSadGTLcVpKGGpPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

09978192-101501

## **FIGURE 214**

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC  
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTAGCTTGGCTGGGCCCCGCTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGGGCCGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTC  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA  
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCCG  
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG  
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC  
TCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCTGGGGTCTCTGCTCCTGCAAGAAAGA  
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATG  
CCCCTGCCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCCTCCTCTTCCTCCTCCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT  
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA  
TCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGCTGCTGCCTGAC  
CCCCAGCACAAATAAAAATGAAACGTG

09978192-101501

## **FIGURE 215**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

09978192-101501  
TOSTOT-26184660

## FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGC  
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG  
GGGACCCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCCTCACCACTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG  
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGCTAGGAGGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTTGGGAGGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG  
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC  
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCT  
GGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAG  
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC  
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG  
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAACGTG

0978192-101501

## FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

09978192-101501

## FIGURE 218

GGTTGCCACAGCTGGTTTTAGGGCCCCGACCACTGGGGCCCCCTTGTGAGGAGAGACAGCCTCCCGCCCCGGGGAG  
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTTCTGCCGTGAGCTGCCGGCCG  
AGTTGGGTCTCCGTGTTTTAGGCCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGCTGGGCCGGTTATCGGGAGG  
AGATTGTCTTCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT  
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGTAAATCGCAAAACCCATTTTGGAGCAGGAATCCAATCA  
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAAAACCTCCAGGCAGGAACACCTTTTGCTGTG  
ATGGCCCGCTCATGATGGCCCGCAAAAGGGCATTTTCTACCTGACCCTTTTCTCATCCTGGGGACATGTACAC  
TCTTCTTCCGCTTTGAGTGCCGCTACCTGGCTGTTTCTGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCT  
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCTAGTGACCCTGGAGTGATTCTCGGGCGCTACCAGATG  
AAGCAGCTTTTATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGCTTCGTA  
TCAAGAATTTCCAGATAAACAACCAGATTGTGAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCC  
GGGCCTCCCATTTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTGGGTGGGGAATTGTG  
TTGGAAGAGGAACTACCGCTACTTCTACCTCTTCTATCCTTTCTCTCTCCCTCCTACAATCTATGTCTTCGCT  
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTGAAAGAACTCCTGGAACCTG  
TTCTAGAAGTCCTCATTTTGCTTCTTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTTCTACTTTCTCGTGG  
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC  
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA  
TTTTGCCACTGGAGGAAAGTGGAAAGTCGACCTCCCACTACTCAAGAGACCAGTAGCAGCCTTTGCCACAGAGCC  
CAGCCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG  
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTTGTGTT  
TAATTAGGGCTATGAGAGATTTTCAAGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT  
GTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACT  
CAAGGCAGTGCCAGAAGATGTGAGTCACTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT  
CCATGGCCTCAGCCACAGGGTCCCCTTGGACCCCTCTCTTCCCTCCAGATCCAGCCCTCCTGCTTGGGGTCAC  
TGGTCTCATTTCTGGGGCTAAAAGTTTTTGGAGTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA  
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAAGACTGAAGAGGAGGGAGAG  
TGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCCAGCATTGCCACAAATCCTTTTAGGAATGGGACAGGTACCT  
TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTTTTGACTCCTGCTCCCATTAGGAG  
CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTTCTCAGAGGAAGCCCAGTGCTCACTTAAAC  
ACTATCCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAACCAAGGCACAGAGAG  
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAAAAATGCTAACCAGTTCTTCCATTAAGCCT  
CGGCTGAGTGAGGGAAGCCAGCACTGCTGCCCTCTCGGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCT  
ATGGTAACCACTGAGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCAGAGCCACTT  
CACCTGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAAGATTTATGT  
ATTATATGTGGCTATATTTCTTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT  
CGGGTGGGGGAGTGTAACCGGAACTTTTTCTATTTGAAGCGATTAACTGTGTCTAATGCA

## **FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYL  
FILSLSLLLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLIFFTLWSVVGLTGFTF  
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPQEAAEA EK

**Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

09978192.101504



## **FIGURE 220**

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT  
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA  
ACATCGT

09978192.101501

## FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATTTT  
TTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA  
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCGGGCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

## **FIGURE 222**

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNIRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYECsasNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGTLQCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKLF

**Signal peptide:**

amino acids 1-28

## **FIGURE 223**

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG

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## FIGURE 224

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA  
ATCACCGCCTGGCCCGACTCCACCATGAACGTGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG  
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT  
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA  
GAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTAC  
CAGTTCTCCTGTGGGGGCTGGATTGCGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC  
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG  
CAGAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGA  
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG  
GCAGTAGCAGGGACCTACAGGGCCACCCATTCTTACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC  
AATGTTATCCAGGTGGACCACTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG  
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG  
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAAACATCACAGTGCCCCAGGACCAGCGGCGCGAC  
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTCT  
CTGTCTTTCTGTGCTGTACCATTTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG  
CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG  
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTCTATGGCACTAAGAAG  
TCCTGTGTGCGGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC  
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG  
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT  
GATATGATTGGTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT  
GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACCTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG  
CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC  
GTCTTCCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATC  
GGTGTGGTCACTGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG  
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAGTACAATCAA  
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG  
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC  
AACCACCAGCTCTTCTTCTGTGGGATTTGCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG  
CTGGTGACCGACCCCAAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCTGCGG  
CACTTTCGGCTGCCCTGTGCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA  
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAA  
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG  
TGCTCTGCTTTGGGGGTGCCCTGCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCGCTGTACCCCT  
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

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## **FIGURE 225**

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH  
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA  
ILKHLLNTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN  
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVLTA  
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLETLTGKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI  
SEIRTA FEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVDGYEISEDSF  
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTRKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLA AFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGLCEVW

**Type II Transmembrane domain:**

amino acids 32-57

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105101 2618166

[illegible]

TTCCCTCCCCCTCCCCCTCCCCCTCCCCCTCCCCCTCC

## **FIGURE 227**

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA  
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC  
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTTCGGA  
GGAACCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGGCCCTGGGACCAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTCAC  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTACCTAGTGAACAACTGCCCCCT  
CCTTTCTTTCTTCTTTTCTTCCCTCCCTCCCTTTCTTCCCCTTTTCTTCCCTTCCCTTCC  
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTTCG  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTTCAGTGTGATGGGTTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCCCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

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## **FIGURE 228**

ATGCCTACTACCTTCCAATAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC  
TTCTATGCCCCGAACCAACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGGC  
ACTTCGGCTGCCCTGTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGT  
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA  
GGTGACATGAGTACAGACCCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT  
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTCACCCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTCCTATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG  
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC  
TGGCTCACCCCTCACGGGCTACCCCCACCTCACCCCTGTGCTCCTTGTGCCACTGCTCCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCAATATGTGTAGCGGGTACTGGTTCCTGT  
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC

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# FIGURE 229

CCCACGCGTCCGAGCCGCCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA  
 GGAGGGGAGGCCAAAAACACCGAAAAACAAAAGAGAGAAACAACACCCAACAACCTGGGGTGG  
 GGGGAAGAAAGAAAGAAAAGAAACCCACCCACCCACCAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG  
 TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG  
 CTGTTGGTGCAGGGTGCTTGTGCTCGAACCAAGTGGCTGGCGGCGGTGCTCCTCAGCCTGTG  
 CTGCCTGCTACCTCCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCTGGGCGGCCGTGG  
 ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT  
 TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTTGCGGGAGGTGATAAGTGGTCAGT  
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG  
 TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTTCAGACTCAACATACACCCAGAACA  
 ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC  
 CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGGCCACTGGGAAACCAGAGCCTTCCA  
 TTTCTTGGCGACACATCTCCCATCAGCAAAACCATTTGAAAATGGACAATATTTGGACATT  
 TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGCAGGAAAATGCTGTGTCATT  
 CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTTCAGGAAATTAAAT  
 CTGGCACCGTGACCCCGGACGCGAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT  
 CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT  
 TCAAAATTTTAGCACAAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA  
 ATTATACCTGTGTGGCTGCCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCT  
 CCAAGTACAGCCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT  
 TGTGTTGACACTGTCCTCTTTTACCAGCATATTCTACCTGAAGAATGCCATTCTACAATAAA  
 TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT  
 GGTACAGTTTGTAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC  
 TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTTTTGATTAGCTACATTA  
 CCTTGTGAAGCAGTACACATTGTCTTTTTTTAAGACGTGAAAGCTCTGAAATTACTTTTAG  
 AGGATATTAATTGTGATTTTCATGTTTGTAACTTACAACCTTTTCAAAGCATTTCAGTCATGGT  
 CTGCTAGGTTGCAGGCTGTAGTTTACAAAACGAATATTGCAGTGAATATGTGATTCTTTAA  
 GGCTGCAATACAAGCATTTCAGTTCCTGTGTTTCAATAAGAGTCAATCCACATTTTACAAAGATG  
 CATTTTTTTCTTTTTTGATAAAAAGCAAATAATATTGCCTTCAGATTATTTCTTCAAATA  
 TAACACATATCTAGATTTTTCTGCTTGCATGATATTTCAGGTTTCAGGAATGAGCCTTGTAAT  
 ATAAGTGGCTGTGCAGCTCTGCTTCTCTTTCCTGTAAGTTCAGCATGGGTGTGCCTTCATAC  
 AATAATATTTTTCTCTTTGTCTCCAATAATATAAAATGTTTTGCTAAATCTTACAATTTGA  
 AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACTATCTCTAAGTAACGAAGGAGC  
 TATTGGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTTGAGAATTTTGCCCCACACT  
 AACTCAGTTCTTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTTCT  
 TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCCTTTAAATGACAGCACA  
 GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCTTTTCACTAGTCCAAGCCAAAAA  
 TTTTAAGATGATTTGTGAGAAAGGGCACAAAGTCCTATCACCTAATATTACAAGAGTTGGTA  
 AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA  
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC  
 AGGAGGAAATTACAGAGACAATTATGACAACCTGAAATGAGACATGCACATAATATAGATACA  
 CAAGGAATAATTTCTGATCCAGGATCGTCTTCCAAATGGCTGTATTTATAAAGGTTTTTGG  
 AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTTAAATTGACCTGCCA  
 AGGTAGCTGAAGACCTTTTAGACAGTTCCATCTTTTTTTTTTAAATTTTTTCTGCCTATTTAA  
 AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 230**

MMLLVQGACCSNQWLAAVLLSLCCLLPSCLPAGQSVDFPWAAVDNMMVRKGD TAVLR CYLED  
GASKGAWLNRSSIIIFAGGDKWSVDPRVSISTLNKRDYSLQIQNVDTVDDGPYTCSVQTQHTP  
RTMQVHLTVQVPPKIYDISNDMTVNEGTVNLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYECSAENAVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV  
PPPAFEWYKGEKKLFNGQQGIIIIQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL  
NPPSTAQYGITGSADVLFSCWYLVLTLSSTFISIFYLKNAILQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 326-345

#### **N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

#### **Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

#### **Tyrosine kinase phosphorylation site.**

amino acids 178-186

#### **N-myristoylation sites.**

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325

#### **Myelin P0 protein:**

amino acids 92-121

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## FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGG  
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA  
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTCGAAA  
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTCTCCCTAGCTGTGGTGGTCATC  
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC  
GCGGCTCCGGGTCCTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT  
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG  
CAAGTCCTGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGTCTGCAGCGGGT  
AGACAACTTCACTCAGAACCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTC  
TTCAAGGTCACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCCGCGGGACCACCTGCT  
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG  
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCCAGGGTGCTCCAGGGAAGCAAG  
GAGCCACTGGCACCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT  
GGCCCAAAGGGGAACTGGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA  
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTATGGGGCCTCCTGGAGCCCAGGGGAGTA  
AAGGTGACTTCGGGAGGCCAGGCCCACCAGGTTTGGCTGGTTTTCTCTGGAGCTAAAGGAGAT  
CAAGGACAACCTGGACTGCAGGGTGTTCCGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGC  
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA  
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA  
AGAAAAGGAGAATCAGGAGTTCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG  
GCTGGCAGGTCCCAAGGGAGCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG  
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC  
GTCAGGATTGTTCGGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG  
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT  
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT  
GTTCAAGTGTGCGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA  
TGACTGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGTCTGAACCCGAAACCCCTTTCA  
CTTCTCTGCTCCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT  
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAGCTCAACATCATTGA

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## **FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPF EINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL  
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR  
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD  
GATGPSGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE  
KGDGLPGSKGDRGMKGDAGVMGPPGAQGSKGDGFRPGPPGLAGFPGAKGDQGPGLQGVPG  
PPGAVGHGPAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTGLQGGQGRKGESGVPGPA  
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGR  
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLW  
SCTKNSWGHHDCSHEEDAGVECSV

### **Transmembrane domain:**

amino acids 47-66 (type II)

### **N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

### **Tyrosine kinase phosphorylation site.**

amino acids 432-440

### **N-myristoylation sites.**

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521

### **Amidation site.**

amino acids 360-364

### **Leucine zipper pattern.**

amino acids 56-78

### **Speract receptor repeat**

amino acids 422-471, 488-519

### **Clq domain proteins.**

amino acids 151-184, 301-334, 316-349

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## FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT  
CTTCTCCTTTTGGCCAAACTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG  
ACCAAAGGAAAGAAGAAAAAGGGCCAAAGCCAAAATGAAACTGATGGTACTTGTTTTTAC  
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA  
GAAAGATACTAAAAGATCACAACTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG  
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTTCG  
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTTC  
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT  
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAAAAAAAAAA

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## FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLG VQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG  
KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 72-76

#### **Tyrosine kinase phosphorylation site.**

amino acids 63-71

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## FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCCAGCCTGCAGGG  
CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGC  
GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATG  
TGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCGCTGGCTGTG  
CGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCTCTTCGGGTGGTTTA  
TAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGAT  
GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC  
AGGAACAGAACAAAACCTTTCAGCTTGCAAAGCAAATTCAATCCCAGTGGAAAGAATTTGGCC  
TGGATTCTGTTGAGCTAGCTCATTATGATGTCTGTTGTCTACCCAAATAAGACTCATCCC  
AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTTGAACC  
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